Total Elapsed 00:00:00:00

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A 100% identical sequence to the query sequence was found:
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                                                                                                                                                                                            The scores below are sorted by initial score.
Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                                         1. US-09-020-747-11 Sequence 110, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-071-710-1 Sequence 1, Application US US-09-525-397-1 Sequence 1, Application US US-08-850-713-1 Sequence 1, Application US
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-071-710-8 Sequence 8,
-071-710-4 Sequence 4,
-525-397-4 Sequence 4,
-850-713-5 Sequence 5,
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                                                                                                                                                                                                                                                                                                                                  Results of the initial comparison of US-09-030-606-110 (1-3410) with:
    File: 6130043.seq
    File: 6252047.seq
    File: USO8806596.seq
    File: USO8850713.seq
    File: USO8904809.seq
    File: USO9020747.seq
    File: USO9041894A.seq
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290 300 310 1540 1550 ACTGGAGGTGCTAGCAGTGAGGAC 	1610 1620 1630 CCTAATGGACACGTGGGTGCTGGA 	680 1590 1700 CTGTGATGTCTCCGTACGTGTGTG	1760 1770 CTGGACCTCGCATCCTGGATAGT 	1830. 1840 TGTCCAGCTCAGCCAGTCTGTCACT	1900 1910 TGCTACACGTAGTATTTGACAAG 	1970 . 1980 1990 GTGGAGGCCTGCCTCACTGGGTCC	2040 2050 2060 CGCCAGTTTCTGTTGCTGCCAAAGTAATG IIIIIIIIIIIIIIIIIIIIIIIIIIIIII	0 2120 2130 CTGGGGGCTGGGGCGTCCCTCTT 	2190 2200 TTTCAGTCTGGACTTATACAGGGAG 	2260 2270 TACCCAGGCTCAGGGTTAACAGCTA [	2340 2350 TGAATAAACTCAGTCACCTGGTTTCCCATC 
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US/09841894A Application (1-3410) Sequence US-09-030-606-110 US-09-841-894A-1 7.03 8 8 11 Significance Mismatches ore = 2129 = 2139 Substitutions Score Optimized Scor Matches Conservative ( 1381 99% 3 Initial Score = Residue Identity = Gaps = =

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AGTCTCTAGGGCTGCCTACCAAGGGGGCCAGAAG         960       970       980       1010       1020       1030         2220       2230       2240       2250       2260       2270       2280         GGCTCCATGCATGCAGTGCACTCTGCAGTGCATTACCCAGGCTTCAGCTTAACAGCTAGCCTCCTA		2510 2520 2530 2540 2550 2560 2570  CACAGCACTGTTTTTGCTGATCCACCCCCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGT	2720 2730 2740 2750 2760 2770 2780 2780 2760 2770 2780 2780 2760 2770 2780 2780 2780 2780 2780 2780 278	2870 2880 2890 2910 2910 2920 2930  TAGAGGTGGCTTCAGGTCTCAACGCTTCCTTTGGCCCAGCCTGGTTCCCCC

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US-08-806-596-10 S
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2160 2170 GGCTGCCTGAGTGGAGGG 10. US-09-030-606-110 (1-3410) US-08-904-809-10 Sequence 10, Application

US/08904809

Initial Score = 554 Optimized Score = 720 Significance = 2.57
Residue Identity = 94% Matches = 745 Mismatches = 41
Gaps = 6 Conservative Substitutions = 0

GGCTGCCTGACTGGAGGCCTTCCAAGGG

2170

2160

.. US-09-030-606-110 (1-3410) US-09-020-747-10 Sequence 10, Application US/09020747 Initial Score = 554 Optimized Score = 720 Significance = 2.57
Residue Identity = 94% Matches = 745 Mismatches = 41
Gaps = 6 Conservative Substitutions = 0

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(1-3410) Sequence 12,

US-09-030-606-110 US-09-841-894A-1

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US-09-071-710-10 8
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US-08-850-713-13 Sequence 13, Application
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US-09-525-397-9 Sequence 9, Application
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US-09-030-606-110 (1-3410) US-08-850-713-10 Sequence 10, Application US/08850713

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US-09-071-710-1 Sequence 1
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32. US-09-030-606-110 (1-3410) US-08-850-713-1 Sequence 1, Application

US/08850713

Initial Score = 256 Optimized Score = 257 Significance = 0.97
Residue Identity = 99% Matches = 257 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

33. US-09-030-606-110 (1-3410) US-09-841-894A-1 Sequence 1, Application US/09841894A Initial Score = 256 Optimized Score = 257 Significance = 0.97
Residue Identity = 99% Matches = 257 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

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34. US-09-030-606-110 (1-3410) US-09-071-710-3 Sequence 3, Application US/09071710 Initial Score = 254 Optimized Score = 254 Significance = 0.96
Residue Identity = 99% Matches = 254 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

35. US-09-030-606-110 (1-3410) US-09-525-397-3 Sequence 3, Application US/09525397

Initial Score = 254 Optimized Score = 254 Significance = Residue Identity = 99% Matches = 254 Mismatches = Gaps = 0 Conservative Substitutions =

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0.94

Significance Mismatches

Optimized Score = 328 Matches = 333 Conservative Substitutions

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US-09-030-606-110 (1-3410) US-09-071-710-8 Sequence 8

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US-09-841-894A-3
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| 140 | 1450 | 1460 | 1470 | 1480 | 1500 | 1510 | 1500 | 1510 | 1500 | 1510 | 1510 | 1500 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1510 | 1

.res

us-09-030-606-110

1860 1870 1880 1890 ATATGGTGTCTCGCCCAGGCCTGGGTCTGGTCATTTACTTT 1840 x 1850 AGTCTGTCACTGCCTAT ||||||||| AGTCTGTCA 240 x 1550 1560 GCAGTGAGGACAGCCT 30

US/09525397 4, Application 10 (1-3410) Sequence 4, 40. US-09-030-606-11 US-09-525-397-4

9200 o. Optimized Score = 247 Significance Matches = 247 Mismatches Conservative Substitutions Optimized Score Matches 247 1008 0 Initial Score Residue Identity Gaps

1620

1770

1840 x 1850
AGTCTGTCACTGCCTAT
|||||||||
AGTCTGTCA

US/08850713 10 (1-3410) Sequence 5, 41. US-09-030-606-11 US-08-850-713-5

92 o. Significance 247 Score Optimized Initial Score

00 Mismatches 1840 x 1850 1860 1870 1880 1890
AGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTT
|||||||||
AGTCTGTCA
240 x = 247 Substitutions Matches Conservative 100% Residue Gaps

(1-3410) Sequence 4, Application US/09841894A US-09-030-606-110 US-09-841-894A-4 2 42.

0.92 Significance Mismatches Optimized Score = 247
Matches = 247
Conservative Substitutions 247 100**8** 0 11 11 11 Score Identity Initial Residue Gaps

1840 X 1850 1860 1870 1880 1890
AGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTAC#TT
|||||||||||||
AGTCTGTCA
240 X

43. US-09-030-606-110 (1-3410)

0.76

Significance Mismatches

Optimized Score = 217
Matches = 217
Conservative Substitutions

us/09525397

Application

2

24

2190 Gaps

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1430 1440 1450
TTCAGCGGCCTCACCGGGTTCACCTTCT
                                                                                                                                                     US-09-030-606-110 (1-3410)
US-08-850-713-2 Sequence 2,
Sequence
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GGGTTCACCTTCT
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US-09-071-710-2 Sequence 2
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TGGACTTATACAGGGAC
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TTCAGCCGCCCTCACC
                                                              CTCAGGGTTAACAGCT
                                                     2270 2
CTCAGGGTTAACAGCT
 US-08-850-713-9
                                                                                                                                                                               Initial Score = Residue Identity = Gaps
        Initial Score = Residue Identity =
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| 1300 | 1300 | 1310 | 1330 | 1340 | 1350 | 1340 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 1350 | 130 | 130 | 130 | 150 | 150 | 130 | 150 | 130 | 150 | 130 | 150 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130 | 130
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US/08850713
                                                                                     Optimized Score = 217
Matches = 217
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(1-3410)

45. US-09-030-606-11

1360

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3070 3080 3100 3110 x 3120 3130
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US-08-850-713-14
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Sequence 14, Application US/09841894A
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Conservative Substitutions
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Conservative Substitutions
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Sequence 8, Application
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FGAGACACCTAGAGAAGG
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Sequence 7,
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US-09-525-397-7 St
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US-08-850-713-8
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Sequence 13,
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Sequence 7
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Sequence 13, Application US/09841894A
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                                                                  Application
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Sequence 5, Application
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Matches
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GGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATT
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US-09-525-397-13
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GGTTTAAGTGCCGTTT
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US-09-841-894A-1
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US-09-071-710-5
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CGAGGCCAGGGTGGTT
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AAAATTTCCCCTACC
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0.28
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                                                                                                                      Significance
Mismatches
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Mismatches
                                                                                                                                                                                                                                                                                                    US/09841894A
                                                                                                            US/09525397
                                                                                                                      ore = 226
= 231
Substitutions
                                                                                                                                                                                                                                                                                                             Optimized Score = 226
Matches = 231
Conservative Substitutions
                                                                                                                                                                                                                                                                         2010 2020 2030 2040 TGTTAGCCCCATGGGGCTGCCGGGCTGCCGAGTTTCTGTTG
                                                                                  2010 2020 2030 2040 TGTTAGCCCCCATGGGGCCGGGCTGGCCGCCAGTTCTGTTG
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Matches
Conservative (
                                                                                                                                                                                                                                                                                              (1-3410)
Sequence 5,
                                                                                                      US-09-030-606-110 (1-3410)
US-09-525-397-5 Sequence 5,
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998
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99%
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US-09-841-894A-5 S
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90 1930 CTTGGCCAA          CTTGGCCAA	x rcccccrcc 111 111 rccc 230	e = 0.17 = 461 = 0 1680 ccrgrgargrc ccrgrgargrc ccraaararraga 20	, ,		2040 CAGTTTCTGTT       CAGGTGACTGA 350 10 GCTGGGGGCTG            CCCTGAGCCTG	2190 3GTTTCAGTCT            AAGTCCAGACT
30 40 50 60 70 80 90  1870 1880 1890 1900 1910 1920 1930  TGCCGCAGGCTGGGTCTGCTCTTTGCTACACAGGTAGTATTTGACAAGAGGGCTTGGCCAA	1940   1950   1960   1970   1980   1990   X   X   X   X   X   X   X   X   X	6 gnificanc smatches 670 GGGCCTCTG 11	### 1700	1840	1980	0         2130         2140         2150         2150         2190           GGGCGTCCTCTCTCTCCCAGTCTCTAGGGC-TGCCTGAGGGGGTTTCAGTCT         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
70 1910 CAGGTAGTATI            CAGGTAGTATI	1980 GCCTGCCTCA( 	Application US/0880659 ed Score = 249 Si tative Substitutions 1650 1660 1 CCACCTCCACCCGCCTCTGCG	1730 174 iGTGGTTCCGGGCC       TTGTTAAATAAA7 70 100 1810 CCCATCCTGTT77                     CATCCTGTT77  ACATCTTGATAAA	1880               TTGTGTGTTGC 210 1950 TAGAAAACTTC           GAGGAGTGTTT 270	2020 ATGGGGCTGCC	CCTGACTGGAGG CCTGACTGGAGG 
60 1900 CTTTGCTACA 	1970 :GGGGTGGAGG 	Applicatic sed Score s vative Subs 1650 CCCACCTCCAC	1720 CGAGGCCAGGGT           CCCTTCTACTTT 60 190 1800 CCCAGGTGCCCC 	1870 TGCCGCAGGC(           GACCTGGTTC' 200 1940 ATACTCAGCG'           AAATCCCATG	2010 :rgrragcccc 2080 :caccrgrgc 111 :Aggrgrgrcr	2150 TCTAGGGC-TGC TL          TCCAGTGCATGG
50 1890 STCGCCATTTA 	1960 rccaccacatt                 rccaccacatt 190 2030	Sequence 11, Applic Sequence 11, Applic 108 Optimized Scc 37% Matches 39 Conservative 1640 1650	1710 17 GGGTGAGCCCACCG I           TAGCAATGGATTCC 0 50 1780 1790 CTTCCTGCTGTCCC 1	1860 ATATGGTGTC' GGGCTGAGGG 190 1930 ACTTGGCCAA	2000 GCTCCCCGCTCC 111   1   1 GCTGCAGGTT 320 2070 GCTCTCTGCTGC   1   1   1 AAACCCTTCTCT	2140 21 CTCCCCAGTCTC          GTCCCGCATTC 450 4
40 0 1880 CCTGGGTCTGG         -CTGGGTCTGG	1940 1950 1960 1970  ATACTCAGCGTAGAAAACTTCCAGCCACTTGGGGTGGAGGGCCTT  1111111111111111111111111111111	-606-110 (3-596-11 Sec -596-11 Sec 1ty = 3-31 1	1700 GGGGGGGGG AGAAAAGCTA 40 70 17 GGAAAGGCCT H H H H H H H H H H H H H H H H H H H	1840 1850 AGCCAGTCTGTCACTGCCT.       AGCAAAAAGACAGTGCTGT 170 180  1910 1920 GTAGTATTTGACAAGAGCG 240 250	1980 1990 2000 TGCCTCACTGGGTCCCAGCTCCCGGCT	0 2130 2140 2150 GGGCGTCCTCTCTCCCCAGTCTCTAGGGC 
30 1876 TGCCGCAGGG         TGCCGCAGG	1940 ATACTCAGC           ATACTCAGC 170 2010 TGTTAGCCC	69. US-09-030-606 US-08-806-596 Initial Score Residue Identity Gaps 1620 16	1690 1700 TCCGTACGTGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTG	1840 AGCCAGTCT       AGCAAAAAG 170 1910 GTAGTATTT AATAACTTT 240	1980 TGCCTCACT         GAGCTACAT   300   GCTGCCAAA           GTTTATTCZ	2120 GGGCGTCC 11   1   1   6 GGTAATCC

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| 3000 | 3010 | 3020 | 3030 | 3040 | 3050 | 3060 | 3050 | 3060 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 3050 | 
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TAAGTGCCGTTTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGA---ATATTTTATACTGTAAGTGAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTGACTTGTCCTCCAACAAA
X
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                                                                                                                                                                                                                                                                                                                                                                                                                        10 2930 2940 2950 2960 2970 2980 2990 GCTGGTTCCCCCCCACTCCCCTCTACTCTTAGGACTGGGCTGATGAAGGCACTGCCCAAAATT
                                                                                                                                                                                                             2200 2210 2220 2230 2240 2250 2260 GGACTTATACAGGGAGGCCAGAGGCTCCATGCACTGGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70. US-09-030-606-110 (1-3410)
US-09-020-747-98 Sequence 98, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score = 147
Matches = 157
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2470 2480 2490 2500 AGGGGGAACAGAACCAGGTCCCCTCAGCC
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358
5
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	  GAACTTGCTCC	X 450.	. •
GTGTATCCTGGTGCCGGCCGTTTATGAACTGACCACCCTTTGGAATAATCT 390 400 410 420 430 TCTGCGA	1 i TGACGCTCCI	440	
GTGTATCCTGGTGCCGGCCGTTTATGAACTGACCACCCTTT 390 400 410 420 TCTGCGA	GGAATAATCT	430	
GTGTATCCTGGTGCCGGCCGTTTATGAACTG7 390 400 410	 	420	
GTGTATCCTGGTGCCGGCCGTT 390 400 TCTGCGA		410	
GTGTATCCTGGT 390 TCTGCGA	GCCGGCCGTI	400	
	 GTGTATCCTGGT	390	TCTGCGA

71. US-09-030-606-110 (1-3410) US-09-020-747-10 Sequence 109, Application US/09020747 Initial Score = 87 Optimized Score = 537 Significance = 0.06
Residue Identity = 40% Matches = 637 Mismatches = 879
Gaps = 69 Conservative Substitutions = 0

 | 870 | 880 | 930 | 930 | 930 | 930 | 920 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930

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870
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30 40 50 60 70 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1310 1320 1330 1340 1350 1350 1360 1360 1370 GTCAT.----GGACCGGCTGGTGCAGCGATTCGGCAGTCTATTTGGCCAGTGTGGCCAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2020 2030 2040 2050 2060 2070 2080 TGGGGCTGCCGGGCTGCCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCTGTGCT
                                                                                                                                                       0.05
471
0
                                                                                                                                                        Optimized Score = 245 Significance = Aatches = 274 Mismatches = Conservative Substitutions =
                                                                                                                      (1-3410)
Sequence 40, Application US/08806596
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                   1480
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                                                                                                                      72. US-09-030-606-11
US-08-806-596-40
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                                                                                                                                                         Initial Score = Residue Identity = Gaps =
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GTCAT----GGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1240 1250 1260 1270 1280 1290 1300 TATGATGAAGGCGTTCGGAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCTGTTCTTCTCTG
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130 140 150 150 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCTCGATGTCAATGGTCTGGAAGCGGCGGCTGTACCTGCGTAGGGGCACACCGTCAGGGCCCACCAGGAA
170 180 190 230
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ACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGGCACCGAGGCCCGGAGACAC
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                                                                                                 1520 1530 1540 1550 1560 1570 1580 TCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCTGATGACCAGCTTCCTGCCAG
                                                                                                                                       TCCCNCCCGNCCTCTGGCCCNTCAAANANGCTTNCACNACCTGGGTCTGCC---TTCCCCCCTNCCTATCT 670 690 710 720 730
                      TCACCITCTCAGCCCTGCAGATCCTGCCCTACAC---ACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGT
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471
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US-09-020-747-40 Sequence 40, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score - 245
Matches - 274
Conservative Substitutions
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                                                                                                                                                                                                                                                                                      GNACCCCNCNTTTGTCTCANTNT 740 750 X
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Residue Identity = Gans
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GCCCTAAGCCTGGAGGTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCAC PTTCGNTCTTGGCTTCTNCTGATGCCCTANCTGGTTGCCCNGNATGCCAANCANCC 470 480 520 TAAANCACCONCTCCTCNTTTCATCTG-----GGTTNTTNTCCCCGGACCNTGG 1450 1460 1470 1480 1490 1510 TCACCTTCTAGCCCTGCAGGGAGAAGCAGGTGT 0.04 510 0 Optimized Score = 269 Significance Matches = 303 Mismatches Conservative Substitutions 74. US-09-030-606-110 (1-3410) US-08-806-596-14 Sequence 14, Application US/08806596 Optimized Score Matches GNACCCCNCNTTTGTCTCANTNT 740 750 X 368 22 1600 540 GGAATTCCCAAATCTC 460 10 640 ATCCCAGGCCCCTGGA ccaanccccggggrcc Initial Score Residue Identity Gaps 530 590 630 U

TGGAGCTCGTCAAAGCCACTCGTGTATTTTTACACAGGCAGCCTCGTCCGACGCGTCGGGGCAGTTGGGGGTG

TGCTCTTCCTCAAAGTTGTTCT X 10 ACCCCAGG---------CNGCGAACCAANCTTGTTTGGATNCGAAGCNATAATCTNCTNTTCTGCTTGGT 530 540 550 560 570 580 0 1070 1080 1080 1090 1100 1110 1120 1130 GCTGCACCAGCTGTGCTGCTGTGCAGCTGAGTGTGCAGTGTGCAGTTGAGTT TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCA 1280 1290 1300 1310 1310 1320 1330 1340 GEGGGCATC-TCCCTGGTCTTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCT 0 640 650 660 670 680 690 700 ATCCCAGGCCCTGGACTTCTGTGGCCAGGTGTGCT 710 720 730 740 750 760 770 TCACTCCACTGGAGGCCCTGCTCTCTGTCTCTGGGACCCGGACCAGGCCTACTACTCTGTCT TGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAG 1500 1510 1520 1530 1540 1550 1560 ACCACCGGGAGAGGAGGTGCTTGCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGC 0.04 510 0 Optimized Score = 269 Significance Matches = 303 Mismatches Conservative Substitutions 75. US-09-030-606-110 (1-3410) US-08-904-809-14 Sequence 14, Application US/08904809 1180 1170 83 368 22 ||||| || CCCACGGGTTCNGNTGGTTNG 1150 Initial Score = Residue Identity = Gaps

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GGACAGCACANTNACTGTNNANCTTTAGNCCNTGGTCCTCNTGGGTTGNNCTTGAACCTAATCNCCNNTCA 590 640 650
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0 320 330 340 340
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390 440 410 420 430 440 450
                                                                                                                                                                                             | 780 | 790 | 840 | 810 | 820 | 830 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 
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1500 1510 1520 1530 1540 1550 1560 ACCACCGGGAGAGAGCAGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGTTAGCAGTGAGGACACT
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800 810 X
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77. US-09-030-606-110 (1-3410) US-08-904-809-11 Sequence 11, Application US/08904809

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2090 2110 2120 2130 x 2140 2150 TGTGCTGCTGCTGCTGCTGCGGGGCTGGGGGCTGGGGGCTTCTCTCTCTCCCCAGTCTCTAGGG
                                                                                                                                                                                                                                                                                                        300 2310 2320 2330 2340 2350 2360 CTAGAGAAGGGTTTTGGGAGCTGATAACTCAGTCACTGGTTTCCCATCTAAGCCCTTAACCTGC
                                                                                                                                                                                                                                                                                                                                               CCCACCCTACCCAAATATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                      2390 2400 2410 2420 2430 ITAGCTCTTGCATGGGAGTTTCTAGGATGAACACTCCTCCATGGGATTTGAACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATAACTITCATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 2520 2530 2540 2550 2560 2560 2570 2580 TGTCTTTTTGCTGATGTGGTCCTTCTGTTGCCATCA
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670 680 690 710
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476
0
 Optimized Score = .252 Significance Matches = .291 Mismatches Conservative Substitutions
  81
36%
35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGCTTCAGGTCTCA
                                                                                                                                                                                                                              2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                       2380
Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2870
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GCGCAAACTATACTTCGCTCGN X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCGTGCGCCTCGCTTTTCCTCCGCAACCATGTCTGACNANCCCGATTNGGCNGATATCNANAAGN
30 40 50 60 70 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            820 830 840 850 850 870 CICCTGCCTGCCCTACCTGGCCCCA----GGAGGAGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGANCAGTCCAAACTGANTAACACACACACACACACAAATCCNCTGCCTTCCANAGTANACTTGAA 100 110 120 150 150 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNTGACCGNGCNNCCCTCCCCCNTCCATNACGANCCNCCCGCACCACNANNGCNCGCNCCCCGNNCTC

320 330 340 350 350 360 370 380
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                                                                                                                                                                                                                0.02
                                                                                                                                                                                                                254 Significance
293 Mismatches
GCAG-----GCCCNCCACCCCNAATNTTGCTGGGAAATTTTTCCTCCCCTAAATTNTTTC 720 740 750 750 760 760 X
                                                                                                                                               US-09-030-606-110 (1-3410)
US-08-904-809-23 Sequence 23, Application US/08904809
                                                                                                                                                                                                                                                          Conservative Substitutions
                                                               2950 2960 2970 CTCCCCTCTAGGACTGGGCTGAAGGC
                                                                                                                                                                                                                                       Matches
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33%
23
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                                                                                                                                                                                                                  Initial Score
Residue Identity
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1380 1390 1400 1410 1420 1430 1440 CTGTGGCTGCCGCTCTCACCGGGT
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14.21

2.48 2.20 2.08

254 191 380

us-09-030-606-110-inv.res

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Results file us-09-030-606-110-inv.res made by tport on Thu 1 May 103 14:53:55-PDT.
                                                                                                                                                                                                                                                                                                                                                                                                                    initial comparison of US-09-030-606-110' (1-3410) with:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388
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                                                                                                                                                                                                                                                                                           compared:US-09-030-606-110' (1-3410)
searched:
/e cutoff:
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-43
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Release 5.4
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Init. Opt. Length Score Score above mean \*\*\*\* 100 900 \* \* \* above mean above mean . mean 484 484 731 731 753 305 305 43 Sequence 43, Application 43 Sequence 43, Application 37 Sequence 37, Application 37 Sequence 37, Application 32 Sequence 37, Application 32 Sequence 32, Application 32 Sequence 15, Application 15 Sequence 15, Application 34 Sequence 15, Application 34 Sequence 171, Application 35 Sequence 37, Application 37 Sequence 37, Application 38 Sequence 37, Application 38 Sequence 39, Application 39 Sequence 39, Application 37 Sequence 38, Application 38 Sequence 2, Application 38 Sequence 39, Application 39, Applicatio Application Application 20, Application 27, Application 27, Application 19, Application 18, Application 18, Application \*\*\*\* 14 standard US-09-020-747-17 Sequence 171 US-09-020-747-17 Sequence 175 US-08-904-809-72 Sequence 175 US-08-850-713-3 Sequence 72, US-08-86-713-3 Sequence 3, A Sequence Sequence Sequence Sequence Sequence Sequence Sequence scores is US-09-020-747-33 S US-08-806-596-2 Se US-09-020-747-2 Se US-08-806-596-20 S US-08-806-596-27 S US-08-906-596-27 S US-09-020-747-53 S US-09-020-747-53 S US-09-020-747-19 S US-09-020-747-19 S US-09-020-747-10 S US-08-806-596-40 S US-08-904-809-43 S US-08-904-809-37 S US-08-904-809-37 S US-08-904-809-37 S US-08-904-809-37 S US-08-904-809-37 S US-08-904-809-37 S US-08-904-809-32 S US-09-020-747-32 US-09-071-710-15 US-09-525-397-15 US-09-841-894A-1 US-08-904-809-34 US-09-020-747-17 US-08-904-809-19 US-08-806-596-18 US-08-904-809-18 US-09-020-747-18 US-09-020-747-10 US-09-525-397-11 US-09-020-747-86 5-08-904-809-39 5-09-020-747-39 5-09-020-747-15 5-09-020-747-10 The list of best Sequence Name

Application Application Application

Sequence

Sequence

sorted by initial score.

The scores below are Significance is calc

Sequence Seguence

2231 2259 2259 380 380 380 380 380 380 443 227 227 227 227 117 117

253 266 266 266 216 238 238

Thu

ATTCCAGTGCATGGAGCCTTCTGGCCTCCAGACTCAAACCCCTTGGAAGGCTCCAGT	1460 1470 1480 x 1490 1500 1510 1520 TGGAAGTTTTCTACGCTGAGTATTTGCCAAGTCGCTCTTGTCAAATACTACTGTAAATGG	Initial Score   = 374 Optimized Score   664 Significance = 13.64     Residue Identity   = 90% Matches   7.01 Mismatches   58     Gaps
60. US-09-841-894A-8 Sequence 8, Application U 342 56 117 0.69 0 61. US-08-904-809-52 Sequence 52, Application 491 55 72 0.65 0 62. US-09-020-747-10 Sequence 103, Application 581 55 201 0.65 0 64. US-09-020-747-10 Sequence 112, Application 751 55 243 0.65 0 65. US-09-020-747-12 Sequence 112, Application 751 55 243 0.65 0 65. US-08-904-809-12 Sequence 10, Application 789 55 271 0.65 0 67. US-08-904-809-10 Sequence 10, Application 789 55 271 0.65 0 67. US-08-904-809-10 Sequence 10, Application 789 55 271 0.65 0 68. US-08-904-809-10 Sequence 10, Application 789 55 271 0.65 0 69. US-08-904-809-10 Sequence 110, Application 789 55 271 0.65 0 0.65 0 US-08-904-809-10 Sequence 110, Application 789 55 271 0.65 0 0.65 0 US-09-020-747-11 Sequence 110, Application US 247 54 93 0.61 0 72. US-09-021-747-14 Sequence 149, Application US 247 54 93 0.61 0 0.72 US-09-121-25 Sequence 2, Application US 247 54 93 0.61 0 0.61 0 0.61 0 0.61 0.61 0.61 0.6	1. US-09-030-606-110' (1-3410) US-08-806-596-11 Sequence 11, Application US/08806596  Initial Score = 388 Optimized Score = 664 Significance = 14.21  Residue Identity = 90% Matches = 701 Mismatches = 58  Residue Identity = 90% Matches = 701 Mismatches = 58  Saps = 13 Conservative Substitutions = 0  FGATCAGCCCAATGACCAGCTATCTCAGGGGACCTGATTGTTGGGGATCCCCCACCTACCCCAATTAGA  TGATCAGCCCAATGACCAGCTATCTCAGGGGACCTGATTGTTGGGGATCCCCCAACTATTAGA  X 10 20	CACCACCAGGAACCTACCATTCCTACTACTACATACATTACATTCATT

Initial S Residue J Gaps

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-110-inv

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Initial Residue Gaps
                                                                                                                  1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2440
                                                    CCCACCCTACCCAAATATTAGA x 10 20
                                                                                                                                                                                                                                                                                                                                                                                   AGGGGCTTANAGATGGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTT 330 350
                                                                                                                                                                                                                                                                                                           700 710 720 730 740 2CAGCTACCCAAATATTAGA
                                                                                                                                                                                                     1480 X 1490 1500 1510 1520
CTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGG
                                                                                                                                                                                                                                                                                   13.64
58
0
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                                                                                                                                                                                                                                                                                    Significance
Mismatches
                                                                                                                                                                                                                                                                        US/09020747
                                                                                                                                                                                                                                                                                  core = 664
701 |
Substitutions
                                                                                                                                                                                                                                                                 ' (1-3410)
Sequence 11, Application
                                                                                                                                                                                                                                                                                   Optimized Score
Matches
Conservative Sub
                                                                                                                                                                                                                       CCCTAAATTNTTTC
                                                                                                                                                                                                                                                                                   374
908
13
                                                                                                                                                                                                                3. US-09-030-606-110
US-09-020-747-11
CGAAGCTGCAGGTTAA
320
                                                                                                                                                                                                     1460 1470
TGGAAGTTTTCTACGC
                                                                                                                                                                                                                                                                                                           680 690
TGATCAGCCCAATGAC
                                                                                                                                                                                                                                                                                  Initial Score Residue Identity - Gaps
                                                                                                                                                                                                                                               CGACCAGA
                                                      1180
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2--AATGTGC
                     CCAAGGCCTGGGCAGGCATANA x 10 20
                                                                                                                                                                                                2.48
494
0
                                                                                                                                                                                                                                                        2500
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Mismatches
                                                                                                                                                                                                                                                        2490
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                                                                                                                                                                                               ore = 254 :
= 276 P
Substitutions
                                                                                                                                                                                                                                                        2480
                                                                                                                                                                                     US-09-030-606-110' (1-3410)
US-08-904-809-15 Sequence 15, Application
                                                                                                                                                                                               Optimized Scommatches
Conservative
                                                                                                                                                                                                                                                        2470
                                                                                                                                                                                               100
35%
13
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                                                                                                                                                                                                Score
Identity
                                                                                                                                                                                                                                                        2450
                                                                                                                                                                           CGACCAGA
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CTGCTGGCTCGGTGGGGCCCCAGCGCTGCCTCCTCAGCCA----CCAGCAGTGTGGCTGCTACGCAGGTGAGGA

GCCAC----AGAAGTCCAGGCCCCAGGCCCAGGGATGAGCAGTGCCAGGCTCCAGGGGCCTGGGATCCGGGC CCTTCGGGAAGAGAG

<u> AGAGGCGGCACATAGGTGATGCCTGCGGCCCAAACACCTCCCAGGCCCAAAGGTTAGCAGGTTGACCAGCAAG</u> TTCCCCNNTNAACAAAGGGCNCTNGCNTTTGAACTGCCCNAACCCNGGAATCTNCCNNGGAAAANTNCCCC 710 720 720 3010

AGCTGGGCTTTCCGGTGCCGCAGCGGCGCTCACCCACGCTCTGGACCATAGTGGGCCGAGGCGGCTAGG 3090

3150 3160 GCTCAGGGGGCCGTTCAGG

)' (1-3410) Sequence 102, Application US/09020747 5. US-09-030-606-110' US-09-020-747-10 St

191 Significance 227 Mismatches Conservative Substitutions Optimized Score Matches 93 45% 27 Initial Score = Residue Identity = Gaps GCCTTCATCAGCCCAGTCCTAGAGAGAGTAGAGGGGGAGTGGAAGTGGGGGGAACCAGGCTGGGCCAAGAAAA 

)' (1-3410) Sequence 106, Application US/09020747 US-09-030-606-110' US-09-020-747-10 Se

2.08 180 Significance 197 Mismatches Conservative Substitutions II H Optimized Score Matches 90 40% 12 H N N Initial Score Residue Identity

TTTTTTTTTTTTAAACATATAAGAAAGCCTTTAATTTTGTCACCATAAACATTATACTCYGATTGCTCACT

7. US-09-030-606-110' (1-3410) US-08-904-809-53 Sequence 53, Application US/08904809 Initial Score = 87 Optimized Score = 167 Significance = 1.95
Residue Identity = 36% Matches = 178 Mismatches = 304
Gaps = 6 Conservative Substitutions = 0

| 20 | 930 | 940 | 950 | 960 | 970 | 980 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 |

1350 1360

ATTACTTTGGCA

. US-09-030-606-110' (1-3410) US-09-020-747-53 Sequence 53, Application US/09020747 Initial Score = 87 Optimized Score = 167 Significance = 1.95
Residue Identity = 36% Matches = 178 Mismatches = 304
Gaps = 6 Conservative Substitutions = 0

780 790 840
TTCCCTTCTACTTTAAATAATAATTTTAAATGCCTGTGTCTCTGTGATGGCAACAGAAGGA
TTCCCTTCTACTTTGTTAAATAATAATTAATTTAAATGCCTGTGTCTCTGTGATGGCAACAGAAGGA

TTCCCTTCTACTTTGTTAAATAATAATTTAACAGGCTAATT
X
10
20

  1350 1360 ATTACTTTGGCA

1270

1260

1250

1240

```
1.83
469
                                         Significance
Mismatches
            Sequence 19, Application US/09020747
                                        Optimized Score
Matches
9. US-09-030-606-110
            US-09-020-747-19
                                   Initial Score = Residue Identity =
```

Conservative Substitutions

AGAGAGCAGCCACGCNCATCCNTCNAGTGCTGNAAAGCCCCNNCCTGTCTACTTGTTTGGAGAACNGCNN GGCGGGGCTGGCCACGCNCATCCNTCNAGTGCTGNAAAGCCCCCNNCCTGTCTACTTGTTTGGAAACNGCNN 280 290 

GGGGAGCTGGGACCCAGTGAGCAGCCTCCACCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 

NAATCCNCCT

)' (1-3410) Sequence 19, Application US/08806596 US-09-030-606-110' US-08-806-596-19 Se 10.

1.79 Significance Mismatches Optimized Score = 231 Matches = 257 Conservative Substitutions 83 34% 26 Initial Score = Residue Identity =

TGGCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGG 

GGGGAGCTGGGACCCAGTGAGGCAGGCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 

CAGGAAGGCACTTCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCTGGCCTCGGTGGG 1670

											:		
<u>.</u>	1770 GGAGCAG WCCCAACN 720		-	1.71 342 0	70 PTTTTTT               30	140 GCTCACT       SCTTTAAA	210 ccccccrc               crrcrccrc	SCACAGAT          GAGAGGT	360 AGCTCCA I CTAGAAA	430 TGGGCAGT     GCTCAAAT 370	500 AAGAGAA       1  ATAATAA	CCTTGGG 	x seeeecc
640	1760 GGGGGAGGTC     CCNNNGCTTTTN	1830 3CCTGG		Significance = Mismatches = =	60 rrrrrrrrrr            rrrrrrrcrc	130 ATACTCTGATT 	200 GGCACTTAAACC GCTTATCT ACTGGCTTATCT	280 SATTCCCAAC           CCTTGCATATT	350 3GTCCTGCAG1         TTTCATGCAA?	410 420 430 AAAGTTGGGGGTAGGGAAATTTTGGGCAGT 	490 CAGGCTGGGCC     FTACGACAGCA	TCAACACCCTAACO TCAACACCCTAACO 	640 FAGGCATTTTG
630	1750 CGCAGAGCGCC I I I CNGGGNAAAAC	1820 SAGGCTTAGGC	US/09020747		50 (TTTTTTT (TTTTTTTT)	120 2ATAAACATTA           3AAGAAACTC )	190 20 TATTGCAAACGO TATTGCAAACGOOOOOOOOOOOOOOOOOOOOOOOOOOOOO	270 TTCTGTGTGAC         TCAAGTACTAC	340 FIGIGCTICIC       NAACCTIIATI	410 GTTGGGGGTAC 	480 rggggggaacc l xaaatcacatt	550 56 CTACCTTCCTTC 	630 3GTCCTGGGTJ 
620	1740 GCAGAGGCCC I NCNTCNNNA( 690	1810 AAGGGAGCTCC	Application U	Score = 214 236 ve Substitutions	40 TTTTTTTTT        TTTTTTTT	110 ATTTGTCACC           GATAGGGCATG 0	180 AAGACGACATT 	0 260 270 280  TGCTCCTGAGTTCTGTGTGAGATTCCCCAAGCACAGAT	330 GAAACCGCACT           GAATTTGTATCA	400 GTAGGGGAAA(   1	470 GGAGTGGAAG      GGAGCTAATAC	GCCCCACCTCT AATAATTAAAGC 480	620 GAATTTCCAA( 
0.	0 1710 1720 1730 1740 1750 1760 1770 CTCACCCACCACCACCACGTACGAGACATCACAGGCAGAGGCCCGCAGAGCGCGGGTGGAGGTGGAGGCAGAG	X 1790 1800 1810 1820 1830 GCCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGAGCTCCAGGCTTAGGGCTGG       NAATCCNCCT	' (1-3410) Sequence 104, App	Optimized S Matches Conservativ	10 20 30 40 50 60 70 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	80   90   100   120   120   130   140   140   17TTTTTTTTTTTAAACATATAAGAAAGCCTTTAATTTTGTCACCATAAACATTATACTCTGATTGCTCACT   1   1   1   1   1   1   1   1   1	150	25 366	20 FGG   + FGT	370 380 400 410 420 430  AACAGGGTTGTGGAGGTGGGGAAAGTTGGGGGTAGGGGGAAATTTTGGGCAGT	440         450         470         480         500           GCCTTCATCAGCCCAGTCCTAGAGGGGGAGTGGAAGTGGGGGGAACCAGGCTGGGCCAAGAAAAAAAA	510   520   530   540   550   560   570	580 590 600 610 620 630 640 x TAACAGCATTTGGAATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCC
610	1720 GTACGGA         GGCCCGG	) SACGTG	(1-34 equenc	81 0 38% M 27 C	20 TTTTT	rataag         	1 CCCGC   ATGCTA	240 AGCTCA(       FTCTCA(	310 FGGACA       SATATA	380 GGTGGGG 	TAGAG	SCGTTG	600 CCATTT
. 009	ACACGI A   	179( GCACC	-110	0 8 0	TTTTT	90 AAACA1     GATCG2	160 ATTCAC      CTCTT2	OCCCTTZ        CATTCT	TGAGAT       TTACAC	36 AGCTG(       TGCAT2	450 CAGTCC ATCCA1 90	520 GGAAGC       AGTACC	0 AATTA1 
	1710 CCACCACC           NCCCCNCC 660	X TGCCTCCA      CNCCT 730	-030-606	Score Identity	10 FTTTTTA	80 ITTTTTT   GAAATGAG	0 TATAAAAT         AATCAAAT	220 230 240 AGAGATAAGACCTCCCTTAGCTCAGGCAGG	300 CTGGGGGC I TTCTCTAT	370 380 36 AACAGGTTGTGGAGCTGGTGGGGAAAG' 	440 CATCAGCC       GTTAAGTT	0 GTGGTTAG   	590 SCATTTGGA
590	CTCACC	X GCCACTGCCTC        NAATCCNCCT	-60-sn	ial Sc due Ic	TTTTT:	řtttt               tttt(	150 TACAGT,   ATAACA,	220 AGAGA:   1  AAGGA!	90 ATACT(   TTTTC] 250	AACAGO       ATAATO 320	, GCCTT( 11 TGTTT( 380	510 GAGGGG'   AA	580 TAACAC

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GTGGTATTTCTGTAAGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TATCTCNACCANTACTCAC
610 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------TGCGCCCCCGCACCGTTCANCTCGCACTTCTCNAANACCATGANGTTGGGCTCNAACCCAC 370 380 410 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1750 1760 1770 1780 1790 1800 1810 CAGAGCGCGGGGTGGAGGGAGGCACCTCCAGCACCCACGTGTCCATTAGGGAAGGGAGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1820 1830 1840 1850 1860 1870 1880 GGCTTAGGGCCTGGCAGGAGGTGGTCATCAGGCTGCTCACTGCTAGCACCTCCAGTGTCCTCGGTAT
                                                                                                                                                 1250 1260 1270 1280 1290 X 1300 1310 GCCTCCAGTCAGGCAGCCCTAGAGAAGAAGAAGAAGAAGGACGCCCCCAGCCTGTGCAGCTAC
                                                                                                        1.67
483
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAATTCACTTTACAAGCATTTATTAGAATGAATTCACATGTTATTATTCCTAGCCCAACACAATGG 520 530 540 550
                                                                                                         Significance
Mismatches
                                                                        12. US-09-030-606-110' (1-3410)
US-08-806-596-40 Sequence 40, Application US/08806596
                                                                                                        Optimized Score - 233
Matches - 270
Conservative Substitutions
                               650 660 670 680 690 AGACCCCAGGAGAAGATTCTGGCAATGATCAGCCCAATGAC
                                                                                                         80
338
43
                                                                                                      Initial Score Residue Identity Gaps
```

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2600 2610 2620 2630 2640 2650 2660 GAGGTAGCCCAGGCCAGGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACAGAACGAGAGITAICCIGGAIAACICAGAGCIGAGTACCIGCCGGGGGCCGC 250 250 250 200
                                      CNTNCCCCCCCNTGNNACCCANCCTTCTANNGNTTCCCNCCCGNCCTCTGGCCCNTCAAANANGCTTNCACN 630 640 650 650 660 670 680 690
                                                                                                                                                                                                                                                                                                                                                                                                                         2310 2320 2330 2340 2350 2360 2370 2380 CCGGCGCCAGGCTGCAGCTGCTGGTGCAGCCGGGGAAGCAGGCCCCAGGTTCCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 2320 2330 2340 2350 2360 2370 2380 CCGGCGCAGGCTGCAGCTGCTGCTGGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAA
               AAGGTGAACCCGGTGAGGCGGCTGAAGCTGTCACCACGGCCACACTGTGGGACAGGCATGTGGCACCGGCA
                                                                                                         2040 2050 2060 2070 2080 2090 2100 GCCACAGGGAAAGCIGCCACACTGGCCAAATAGACTGGTCGAGTGCCGAATCGCTGCACCAGCCGGTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATCTTTGTTACAGTCTAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2390 2400 2410 2420 2430 2430 2450 AGCCAAGCGGGCCCATCTGCTGGCTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGTTCTTAAATCACCATTCCTTGCTCCTCACCCTCCAGGGTGGTCTCACACTGTAATTAGAGCTATT
30 40 50 90 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATCTTTGTTACAGTCTAAGA
                                                                                                                                                                                                                                                                                                                                                     1.55
                                                                                                                                                                                                                                                                                                                                                           11 0
                                                                                                                                                                                                                                                                                                                                                       Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 Significance 110 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2670 X 2680 2690 2700 2710 2720 GTCCCGGAAGAGGTCAGAGGCCCTCCAGTGGAGTGAAGCACACCTGGCCA
                                                                                                                                                       ACCTGGGTCTGCCTTCCCCTNCCTATCTGNACCCCNCNTTGTCTCANTNT 720 730 740 750 x
                                                                                                                                                                                                                                                                                             13. US-09-030-606-110' (1-3410)
US-08-904-809-43 Sequence 43, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0' (1-3410)
Sequence 43, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 102
Matches = 110
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score
Matches
                                                                                                                                                                                                                      2110 2120 2130 ACCAGAGAGAGACCACTG
1990
                                                                                                                                                                                                                                                                                                                                                    77
34%
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
34%
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14. US-09-030-606-110
US-09-020-747-43
                                                                                                                                                                                                                                                                                                                                                    Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score
Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGAA
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
```

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CACTGGGGAAATGGATGCGTGGAGCTCGTCNAANCCACTCGTGTATTTTTCACA--NGCAGCCTCCTCCGA 160 170 180 190 200 210 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2390 2400 2410 2420 2430 2440 4 2450 AGCCAAGCGGGCCCGCCATGGACAGCGGGCGACAGCCGACAGCCGTTCTGCTGGTCGGT
                                     2600 2610 2620 2630 2640 2650 3660 GAGGTAGCCCAGGCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCT43CGACAGTGGTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2830 2840 2850 2860 2870 2880 2890 AAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGCCGGCGGCGGCGGCCATAGCGTCCACGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATGCTCTTCCTCAAAGT X 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 2980 2990 3000 3010 3020 3030 3040 ATGAACTTCTCCTCTACCCCACTTCCAGCAGAGGGGGCACATAGGTGATGCCTGCGGCCAAACACACC
                                                                                                                                                                                                                                                                                                                                                              TCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGGGGGGTTCACCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3120 3130 3140 3150 3160 3170 3180 AGCCICTGGACCATAGTGGGCCGGTAGGGCTCAGGGGGGCCGTTCAGGCCACTCCAGAACTGCTTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTCCTT-----GCTGCCGCCAACTGCCTAGGAATCAGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGGGTGGGCTGACAGGTGCCAGAACACACTGGATNGGCCTTTCCATGGAAGGGCCTGG5GGAATCNCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 157 Significance = Matches = 185 Mismatches = Conservative Substitutions = -
                                                                                                                                                                               150
                                                                                                                                                                                                                                                                                                                                                                                                                            2670 X 2680 2690 2700 2710 2720 GTCCCGGAAGAGGTCAGAGGGCCTCCAGTGGAGGAGCACACCTGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0' (1-3410)
Sequence 37, Application US/08806596
                                                                                                                                                                                                                2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
338
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-030-606-110'
US-08-806-596-37 Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGGGATGCTCTCCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Score Residue Identity Gaps
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•	•			
360	3260 3290 3310 CGCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTG	3320 3330 3340 3350 3360 3370 3380  CTGTGGGGCACCTCAGTCGTCTCATCACTCAGATCCTGGCCGCGCGCG	3400   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   3410   350	
350	3300 CAGCCCATGC7 	3370 AGGCGCGCGCGC 	TGCNAAGGNAAT 560	
340	3290 STCCAGCTTCT        SGACAGGCTAG	10 3360 CTCAGATCCTGGCCG 	CTTGTTTGAAT 550	•
330	3280 TTTGGTGCCGC 11 11 TTGCACACCCC	3350 TCATCACTCAC 1   1   CANCAAACCAA	NGNGANCCNCC 540	
320	3270 AGCCC             	3340 3GGACACGTC           2AAGCANCCTC 460	3410 STTCCC INAAACCCGCC	
310	3260 CGCCCATTTCTGCC                     NANCCCAAACTGCCTCTC 370 380	3330 SCACCTCAGTG 1 1 PCTTGTTGCCC 450	390 3400 3410 CCAGCGCGTGCAGGCTGGTTCCC 	
300	3260 CGCCCATT'     NANCCCAA	3320 CTGTGGG(       TAGTTGT' 440	3390 CCAGCGC   1   NTACCAN	E

16. US-09-030-606-110' (1-3410) US-08-904-809-37 Sequence 37, Application US/08904809

CGCCCATTTCTGCC---

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GCATGCTGTTTCCTCAAAGT X 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGTTGTTGTTGCCCAAGCANCTCCCANCAAACCAAAANCTTGCAAAAATCTGCFCCGTGGGGGTCATNN
NTACCANGGTTGGGGAAANAAACCCGGCNGNGANCCNCCTTGTTTGAATGCNAAGGNAATAATCCTCTGTC
0 520 530 x 540 550 550 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3050 3060 3070 3080 3090 3100 3110 TCCAGGCCAAAGGTTAGCAGGTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGGGGGCTCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTGGGGAAATGGATGCGGGGGCTCGTCNAANCCACTCGTGTATTTTCACA--NGCAGCCTCCTCGA 180 190 200 200 210 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2830 2840 2850 2860 2870 2880 2890 AGAGGCTCAGGAGGCCCAGGCGCGCGCCATAGCGTCCACGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---recadadrecrerereredenderecangementer 110 120 130 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3120. 3130 3140 3150 3160 3160 3170 3180 AGCCTCTGGACCATAGTGGCGGGTAGGGCTCAGGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTGGGTGGCTGACAGGAACACACTGGATNGGCCTTTCCATGGAAGGCCTGGGGGAAATCNCCT 300 310 320 330 340 350 360
                                                                                                                                                                                                                                                                                                                                              1.55
333
0
                                                                                                                                                                                                                                                                                                                                           Optimized Score = 157 Significance
Matches = 185 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                       17. US-09-030-606-110' (1-3410)
US-09-020-747-37 Sequence 37, Application US/09020747
                                                                                                       3390 3400 3410 CCAGCGCGTGCTGCTTCCC
                                                                                                                                                                                                                                                                                                                                            77
338
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGGGATGCTCTCT----
                                                                                                                                                                                                                                                                                                                                            Initial Score = Residue Identity = Gaps = =
```

	E.	18. US-09-030-606-110' (1-3410) US-08-904-809-32 Sequence 32, Application US/08904809	Initial Score = 74 Optimized Score = 264 Significance = 1.42 Residue Identity = 35% Matches = 281 Mismatches = 499 Gaps = 11 Conservative Substitutions = 0	X 10 50 70 70 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT

150 160 TACAGTATAAAATATT

TITITITITITITAAACATATAAGAAAGCCTTTAATTTTGTCACCATAAACATTATACTCTGATTGCTCACT

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GCCTTCATCAGCCCAGTCCTAGAGAGAGTAGAGGGGAGTGGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 340 350 350 360 360 360 340 350 360 ARACTCTGGGGGCTGAGATGGACAAAGGCTTGGGAAACCGCACTTTGTGCTTCTGGTCCTGCAGTAGCTCCA
                                                                                                                                                                                                                                                              150 160 170 180 190 200 210 TACAGTATAAAATAAATAAATAAAGACGACATTATTGCAAACGGCACTTAAAACCCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTTTTTTTTAAACATATAAGAAAGCCTTTAATTTTGTCACCATAAACATTATACTCTGATTGCTCACT
                                                                                                                                                                                                                                                                                                                                                                          CCNTCCTNNNCACCATCCCCCCNNGNNACGNCTANCAANGNATCCC--TTTTTTTTANAAACGGGCCCCCCNC 740 770 780
GATTGTTGGGGGATCCCCCACCCTACCCAAATATTAGACACCAACACAGAAAAGCTAGCAATGGATTCCCTTC
                                                                                                                                                                  )' (1-3410)
Sequence 32, Application US/09020747
                                                                    X 790 800 810 820 830
TACTITGTTAAATAATAATATATTTAAATGCCTGTGTCTCTGTGAT
                                                                                                                                                                                                                               Conservative Substitutions
                                                                                                                                                                                                      Optimized Score
Matches
                                                                                                                                                                                                        74
358
11
                                                                                                                                                                  US-09-030-606-110'
US-09-020-747-32 S
                                                                                                                                                                                                            H H H
                                                                                                                                                                                                          Initial Score
Residue Identity
```

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20. US-09-030-606-110' (1-3410) US-09-071-710-15 Sequence 15, Application US/090 Initial Score - 73 Optimized Score - 680 Significance - 1.38
Residue Identity - 36% Matches - 809 Mismatches - 1324
Gaps - 101 Conservative Substitutions - 0

 350 360 370 380 390 400 410 CCTGCAGTAGCTCCAAACTTGGGGGTAGGG TAGGGGTAGGG TAGGGGTAGGG TAGGGGTAGGG TAGGGGTAGGG TAGGGGTAGGG TAGGGGTAGGG TAGGGGTAGGG TAGGGGTAGGG TAGGG TAGGGTAGGG TAGGGTAGGG TAGGGTAGGGTAGGG TAGGGTAGGG TAGGGTAGGG TAGGGTAGGG TAGGGTAGGC TAGGGT TAGGCCAGTGTGGCCAGTGTGGCCGTGGT TAGGGT TAGGGT TAGGGT TAGGGT TAGGGT TAGGT TAGGGT TAGGT TAGGGT TAGGT TAGGGT TAGGT TAGGGT TAGGGT TAGGGT TAGGGT TAGGGT TAGGGT TAGGT TAGGGT TAGGT TAGGT TAGGT TAGGT TAGGT TAGGT TAGGT TAGGGT TAGGT T

   | 1500 | 1510 | 1520 | 1530 | 1540 | 1550 | 1560 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 | 1500 |

2360 2370 2380 2390 2400 x 2410 2420 geggaagcagcaccaggttccgaaagccaaagccaacagcaccagaagcagaag 3GGCTTCAGGTCTCAACGCCTTCCTTGGCCCAGCCTGGT 1690 1700 1740 110 2220 2230 2230 2240 2250 2250 2270 2280 CTCTGGGCACGCCCTGGTACAGCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1930 1940 1950 1960 1970 1980 1990 AGGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGGTGAACCCGGTGAGGGGGGGCGCTGAAGCTGTC 0 2020 2030 2040 2040 2050 2060 2060 2060 20GGACAGGGAAAGCTGGCCAAATAG ----ccctctactctcttaggactgggctgatgaaggcactgcccaaatt
1760 1770 1780 TCCCCTACCCCCAACTTTCCCCCAACTTTCCCCAGCTCCACAACCCTGTTTGGAGC-TACTGC 1810 1820 1830 1840 1850 1850 780 1790 1800 1810 1820 1830 1840 1850 CCTCCAGCACCACCAGGAAGGGAAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGG -----AGAATCTTCTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCAGGA 1570 1580 1590 1600 GIGITGGIGTCTAATATTTGGGTAGGGTGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTG (1480 1590 1500 1500 1510 1520 1530 1540 1640 1650 1660 1670 1680 1690 1700 GCACTATCCAGGATGCCAGGAGTCCAGGAGTCCAGGCAGATGCCCCGGCCCGGAACCACCTGGCTCGGTGGGCTCACCC ACAGACTGGCTGGGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGAC rccccacirccaci-2000 2010 ACCACGCCCACACTGT GGCTGATCATTGCC--1550 1580 1780

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570 580 590 600 610 620 630 CACCCTAACCTTGGGATTTTGGGATGAGTATTTCCAAGGTCCTGGGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 650 660 670 680 690; 700 GCATITIGGGGGGGCCAGACCCCAGGAAGAATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACCTGATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAAACACAGAAAAGCTAGCAATGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTA----ATGGACAC 380 390 400 410 420 1 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 500 510 520 530 540 550 560 GCTGGGCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAAGCCCTGAAGCCCTCTACCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACCACGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAG------GGGACACTGGAGGTGCTAGCAG 310 350 350 360
                                                                                                                                                                                                                             ACCAGGGCGTGCCCAGAGCTGA X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 360 370 380 390 400 410 CCTGCAGTAGCTCCAAACATGTGGGGGAAAGTTGGGGGTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 430 440 450 460 470 480 gaattitgggcagtgccttcagtcctagtcctagagagagtagaggggaggggaaccag
                                                                                                                                                                                                                                                                                                                                  GCCGGGCACCGAGGCACACTATGATGATGAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTG 30 40 50 50 60 60 70 80 80 90
                                                                                                                                                                                                                                                                                                                                                                                     140 150 160 200 TCTGATTGCTCACTTACAGTATAAATAAATAAGACGACATTATTGCAAACGGCAC
                                                                                                                                                                                                                                                                                        8 11
                                                                                                                                    680 Significance
809 Mismatches
                                                                                        US-09-030-606-110' (1-3410)
US-09-525-397-15 Sequence 15, Application US/09525397
                                                                                                                                                                   Conservative Substitutions
                                                                                                                                      Optimized Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740
                            2430 2440 2450 GGGCCGACAGCCCTTCTGCTGGCTCGGTGG
2120
                                                                                                                                        73
36%
101
2110
                                                                                                                                         II II II
                                                                                                                                    Initial Score
Residue Identity = Gaps
```

CCCTTCTACTTTGTTAAATAAATAAGTTAAATATTTAAATGCCTGTGTCTCTGTGATGGCAACAGAAGGACC

								•	•			
850         860         870         880         900         910         920           AACAGGCCACATCCTGATAAAAGGTAAAGGGGGGTGGATCAGCAAAAAGACAGTGCTGTGGCTGAGGGGA         1	930 940 950 960 970 980 990 CCTGGTTCTTGTGTGTGCCCTCAGGACTCTTCCCCTACAATAAGTCATATGTTCAAATCCCATGGAGGA	1000 1010 1020 1030 1040 1050 1060 GTGTTCATCCT-AGAAACTCCCATGCAGGCTACATTAAACGAAGGTTAAGGGGCTTAGAGATG	1070 1080 1090 1100 1110 1120 1130 GGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGC	1140 1150 1160 1170 1180 1190 1200 TGTTAACCCTGAGCCTGGGTAATCCACTGCATGCATGGAGCCCTTCTGGCCTCC	1210	1290	1360	1430 1440 1450 1460 1470 1480 1490 CCAGTGAGGCCGTCCACCCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGTTTG	1500   1510   1520   1530   1540   1550   1560   1570   1280   1290   1310   1310   1320	1570   1580   1590   1600   1610   1620   1630   ACAGACTGGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCCACCTGGGACAGCAGGAAG   11111   1   1   1   1   1   1   1	1640   1650   1660   1670   1680   1690   1700   1600   1600   1700   1600   1600   1600   1700   1600   1600   1600   1700   1600   1410   1   1   1   1   1   1   1   1   1	0521 0521 0521 0721

1740

1720

```
GTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTG
1480 1490 1500 1510 1520 1530 1540
                                                                                                                         TCCCTACCCCAACTTTCCCCAACTTTCCCACAGCTCCACAACCTTTGGAGC-TACTGC 1810 1820 1830 1840 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 1790 1800 1810 1820 1830 1840 1850 CTCCAGCACCCACGAGCTCATCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 150 160 170 180 190 200 TCTGATTGCTCACTTACAGTATAAAATAAATAAATAAGACGACATTATTGCAAAACGGCAC
                                                                                                                                                                                                                                                                                                                                     2070 2080 2090 2100 2110 2120 2130 ACTGCTCGAGAGAGAGACCAGGGAGATGGCGCACTGC
ACCACCACACGTACGGAGACATCACAGGCAGAGGCCCCGCAGAGCGCGGGGTGGAGGTGGGAGACAGGCCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        680 Significance
809 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22. US-09-030-606-110' (1-3410)
US-09-841-894A-1 Sequence 15, Application US/09841894A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCAGAGTATAATGTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTA
2100 2110 2120 2130 2140 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score = 680
Matches = 809
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2430 2440 2450 GGGCCGACAGCCTTCTGCTGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
36%
101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial Score
Residue Identity Gaps
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		:			
AGCTGA 20	270 TGAGATT      TGCAGTG 90	0 TCTGGT       TCTATT	GTAGGG   1   CGTGGT 230	GAACCAG    ccrcccr 300	560
ACCAGGGCGTGCCCAGAGCTGA X 10 20	210 220 240 250 250 270  TTAAACCCCCCTGAGATAAGACCTCCCTTAGCTCAGGCAGG	280 330 340 340 320 320 330 340 340 ccca-agcacagatatactcrgggggcrgagatggacaaaggctrgggaaaccgcacttrgrgctrrggt	350 360 410 410 CCTGCAGTAGCTCGAAAGTTGGGGGTAGGGGAAAGTTGGGGGTAGGG GTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGTAGGGGGTAGGGGTAGGGGTAGGGGGTAGGGTAGGGCTAGCCAAGTGTGGGCGTGGTAGAGTGTAGGCTAGGCGTAGGTGTAGGCTAGGCGTAGGTGTAGGCTAGGCTAGGCGTAGGTGTAGGCTAGGCGTAGGTAG	420 430 440 450 460 470 480 GAAATTTTGGGCAGTGCCTTCATCAGCCCAGTCCTAGAGAGTTGGGGAGTGGGGGGAACCAG	7.50
ACCAGG( X	250 26 GGTGCTCCTGA( 	330 3GGAAACCGCAC I II IIII 3CGATTCGCCAC	400 segeracees       recereree	470 GAGGGAGTGG     GATCCTGCCCT	0.4.0
	CAGGCAGGGGG CAGGCAGGGGG I I I I I CGTTCGGATGG	320 CAAAGGCTTGG           CTGGTGC-AGC	390 GGAAAGTTGG I CACA	460 SAGAGAGTAG, I II AGCCCTGCAG,	000
	240 CCTTAGCTCAC CCTTAGCTCAC IGATGAAGGCG	310 GCTGAGATGGA G	350 360 370 380 CCTGCAGTAGTGGGGGGAAACAGGGTTGTGGGGGGTGGTGGGGAAACAGGGTTGTGGGTGG	450 ccagrccraga(   1   1   caccrrcrcago	
	230 ATAAGACCTCC   1   SAGACACTATC	300 SATACTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	370 AGGGTTGTG(     TCCCTGTGG(	440 TTCATCAGCC	(
	220 CCCTGAGAGA         CGAGGCCCG	290 ACAGATATA         CCTGGTCTT	360 GCTCCAAAC     TGGCAGCTT	430 3GGCAGTGCC1        2AGCCGCCTC	
	210 TTAAACCCC       GCCGGGCAC	280 CCCCA-AGC         CGCCATCTC	350 CCTGCAGTA      TGGCCAGTG	420 GAAATTTTG         GACAGCTTC	

			• :
260	ccttcaa 	630 GGGTTAG      TGGACAC 430	700 ATCTCAGG       ATGTCTCC
550	GCTGGGCCAAGAAGAGGGTGGTTAGGGAAGCCGTTGAGACCTGAAGCCCCACCCTCTACCTTCTTCAA 	570         580         590         600         610         620         630           CACCCTAACCTTGGGATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAG         1	ACCAGCT
540	CCCCACCCTC:       -GGGACACTG( 350	GAATTTCC	690 AGCCCAATG2 
	ACCTGAAG	610 GATGAGTAC     CTGGAGCTC	680 AATGATCA
530	GCTGGGCCAGAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGACC 	590 600 610 620 TGGAATTATCATTTGGGATGAGTAGAATTTCCAAG	670 ATTCTGGC
520	SAAGAGGGTGGTTAGGGAAGCCG                  SAAGCAGGTGTŤCCTGCCCAAATAC	590 TGGAATTA    CTGCCAGG	660 GAGAAGAAG
510	sectect    Aegretre	70 580 590 ACCTTGGGTAACAGCATTTGGA 	10 650 60 FTGGGGGGCCAGACCCCAGG
90	GCCAAGAGAAGAGGGG                       ACCGGAGAAGCAGGT	SCTTGGGTA	650 GGGCCAGA 
	TGGGCCAU	570 CACCCTAACCT 1 1 TGAGGACAGCC 370	640 CATTTTGG
007	, is 5	3 H C	ŏ − ĕ

GTGGGTGCT 440	GGAGGCAGTC 450	SGCCTGCTCCC	ACCTCCACCG 470	480 480	666CCTCTGC 490	GIGGGIGCIGGAGGCAGIGGCCIGCICCCACCCGCGCGCTCIGCGGGGCCICIGCCIGIGAIGICICC 440 440 450 450 460 450
710	720	730	740	750	760	770
GGACCTGAT	FTGTTGGGGA	TCCCCCACCCT	ACCCAAATATI	AGACACCAA	CACAGAAAAG	GGACCTGATTGTTGGGGGATCCCCCACCCTACCCAAATATTAGACACCCAACACAGAAAAGCTAGCAATGGAT
	)   			GGTTCCGGG	CCGGGGCATC	
510	520	530	540	550	260	570

-GATTTGAACATA

	180   790   800   810   820   830   840   820   830   840   820
	820 GCCTGTGTCTCTGTGATGG                       ATCCCTGTTTATGGGCTCG620
) )	820 AATGCCTGTG CCCATCCCTG
1	810 AAATATTTAI 
2	800 ATAAATAAGTT           1 TTCCTGCTGTC 600
9	790 ACTTTGTTAA   11 GGATAGTGCC 590
076	780 CCCTTCT 11         CCATCCT 580

<sup>| 850 | 860 | 870 | 880 | 890 | 900 | 910 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920</sup> 

830 840	1070	1140	10         1230         1240         1250         1260         1270         1280           CTGTATAAGTCCAGACTGAAACCCCTTGGAAGGCCTCCAGTCAGGCACTGGGAGAGGAAGGA	1290	1360 1370 1380 1390 1400 1410 1420 ACTITGGCAGCAACAGAAACIGGGGCAGCCCGGCAGCCCAIGGGGCTAACAGGAGCGGGGAGCTGGGAC	1430 1440 1450 1460 1470 1480 1490 CCAGTGAGGCAGCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTG
820	1100 CCAAAAACO L TGTGGCTCT 880	1170 GCAGAGTCCC 	1240 GGAAGGCCTCC                GGGAGGCCAGA	1320 TACGCACCTC/ 	1390 SCCCGCAGC 	1460 SCTGGAAGTI
810	1090 TTTATTCAGCTC 	1160 GTAATCCACCTG            GGCGTCCCTCTC 940	1230 124( GAAACCCCTTGGA/ 	1300 CCCCAGCTGTGCAGCT 	1360 1370 1380 1390 1 ACTTTGGCAGCAAACTGGCGGCCAGCCCGGCAGCCCATG 	1450 CACCCAATGT
800	1080 STGACTGAG'     TTTCTGTTG	1150 TGAGCCTGG 	1220 AGTCCAGACTG           GTTTCAGTCTG	0 130( CCCAGCCCCC/             CCCAGGCTCA(	1370 IGCAACAGAAA       AACTCAGTCAC	1440 3CAGGCCCTC
790	1070 GGAAACCAG(            GGCGCCAG' 850	1140 TGTTAACCC          TGCACAGCT	1210 CTGTATAAG       CAAGGGGT   990	1290 GAGGGACGCC    - - - GGTGGATTAC 1070	1360 ACTTGGCA       GCTGAATAP	1430 CCAGTGAGG

GGGCCGACAGCCCTTCTGCTGGCTCGGTGG

23. US-09-030-606-110' (1-3410) US-08-904-809-34 Sequence 34, Application US/08904809 Initial Score = 72 Optimized Score = 253 Significance = 1.34
Residue Identity = 38% Matches = 304 Mismatches = 451
Gaps = 45 Conservative Substitutions = 0

3200

., 24. US-09-030-606-110' (1-3410) US-09-020-747-17 Sequence 171, Application US/09020747 Initial Score = 71 Optimized Score = 419 Significance = 1.30
Residue Identity = 37% Matches = 481 Mismatches = 761
Gaps = 37 Conservative Substitutions = 0

GGACTGCAGCCCGCACCCTGGCAGGCGCCACTGGTCATGGAAAACGAATTGT-TCTGCTCGGGC 30 80 90	
ACGAATTGT-TC . 80	
STCATGGAAA 70	
GCGGCACTGC 60	
SCCCTGGCAG 50	
GCACTCGCA( 40	
GGACTGCAGCCC 30	

| 2420 | 2430 | 2440 | 2450 | 2460 | 2470 | 2480 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2470 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 | 2480 |

 | 3060 | 870 | 880 | 890 | 910 | 4920 | 310 | 310 | 3120 | 3120 | 310 | 3100 | 3110 | 3120 | 3120 | 3100 | 3110 | 3120 | 3120 | 3120 | 3120 | 3120 | 3120 | 3120 | 3130 | 3140 | 3150 | 3140 | 3150 | 3140 | 3150 | 3140 | 3180 | 3140 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 | 3180 |

25. US-09-030-606-110' (1-3410) US-09-020-747-17 Sequence 173, Application US/09020747 Initial Score = 71 Optimized Score = 426 Significance = 1.30 Residue Identity = 38% Matches = 490 Mismatches = 756 Gaps = 0

 2810 2820 2830 2840 2850 2860 2870 CAGCCGGCCCTTGGGAAGAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGG 3100 3110 3120 3130 3140 3150 3160 CGCAGCAGGCGGCTCAGGGGGGCCCGTTCAG io 2460 2470 2480 2490 2500 2510 2520 GIGGGCCCCAGCGCTCCTCAGCCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAG GGGCCCCTGATCTGCAACGGGTACTTGCAGGCCCTTTTCGGAAAAGCCCCCGTGTGGCCAAGTTGG 3030 3040 3050 3060 3070 3080 3090
ATGCCTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGC CTTGTGGNANGTTGACCCAACCTTACCAGTTGGTTTTTTCATTTTTNGTCCCTTTCC 2330 2340 2350 2360 2370 2300 2300 2370 26GGGCATGCTGCTGCTGCTGCGGGAAGCAGGCCCCAGGTTCCGG 510 2620 2630 2640 2650 2660 GCCACCCCAAGACTGATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT 2670 2680 2680 2700 2710 2710 2720 2730 CCGGGTCCCGGAA---GAGGTCAGGGCCTCCAGTGGAGTGAAGCACCTGG-CCACAGAAGTCC 750 2760 2770 2780 2790 2800 AGGATGAGCCCTGCTAGC 2880 2890 2900 2910 2920 2930 2940 CGGCCATAGCGTCCACCAGCTCACTGGACCGGGACACAGACCAGGCCCAGCACTGGA ----CCAATGCCACCTAGATTTTCCCTGNA 1130 NAGGTCCCAGCCCTCTTCCNTCAGACCCAGNGGT----AGCAGCCCACGCCCAG 2310 2320 AGCCGGCGCAGGGTGC CACAG----TGCCCC 2600 26 GCAGGAGGTAGCCCAG GGCCCCCAACCCCTCC 1030 2670 2380

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CATGCTCATCAAGTTGGACGAATCCGTGTCTGACATCCGGAGCATCAGCATTGCTTCGCAGTG 240 250 260 260 300
                                                                                                                                                                                                                                                                                                   GTTTCAGAACTCCTACACCATCGG-----GCTGGGCCTGCACAGTCTTGAGGCCGACCAAGAGCCAGG 130 140 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2310 2320 2330 2340 2350 2360 2370 GCCGGCGCAGGCTGCAGCTGGTGCAGCCGGGGAAGCAGGCCCCCAGGTTCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 2460 2470 2480 2490 2500 2510 2520 GGTGGGCCCAGCCTCCTCAGCCAGCAGCAGCTGCTACGCAGGTGAGGAGATGAGGGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCAGAATGCCTACCGTGCTGCGTGAACGTGTCGGTGTCTGAGGANGTCTGCAGTAAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2170 2180 2190 2200 2210 x 2220 2330 GAACGCCTTCATCATAGTGTTCTCGGGCCTTCGGTGCCCGGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGAGGTAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCCAAGCGGGCCCGGCATGGACAGCAGTGGGGGCGACAAGGAGGGGGGCCGA--CAGCCCTTCTGCTGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGTCCCGGAAGAGGTCAGAGAGCAGGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGAGTCCAGGAG
                                                                                                                                                                                                          1.26
695
0
                                                                                                                                                                                                          Significance
Mismatches
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                                                                                                                                                              US-09-030-606-110' (1-3410)
US-09-020-747-17 Sequence 175, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2430
                                                                                                                                                                                                         Optimized Score = 392
Matches = 457
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2640
                                                     2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2700
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         3190
                                                                                                                                                                                                      70
378
60
                                                                                                 3240 3250 CTAGGAATCAGCCAGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2400
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                                                                                                                                                                                                       Initial Score
Residue Identity
Gaps
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----GGCTTCC 70
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3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 3220 | 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATTCAGGAATATCTGTTCCCAGCCCTCCTCCTCAGGCCCAGGAGTCCAGGCCCCAGCCCTCCTCCC 700 710 720 730 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2960 2970 2980 2990 3000 3010 3020 GCCCAGCACCATGCACCATTCTACCCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGCC
2810 2820 2830 2840 2850 2860 2870 2880 GGCCCTTGGGATGAGAAGAGCCTCAGGTGCCCAAAGACACTGCCCAGATGAAGGGCCGGCGGCGGCCG
                                                                                                                                                              Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27. US-09-030-606-110' (1-3410)
US-08-904-809-72 Sequence 72, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Optimized Score = 170
Matches = 197
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATTCAACTANCAAAGAANACTGCTTCAGGGCGTGTAAAATGAAA---330 40 50 60
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36%
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCCGCAGCAGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCAACACCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACCCAGGGGTGCAGG
                                                                                                                                                                                                                                        AAGCCCGTGTGGCCA
560 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score Residue Identity Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         770
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1990 2000 2010 2020 2030 2040 2050
GGCTGAAGCTGTCACCACACACCACACAGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTGGGGCTGTTCCTGCAGTG X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1850 1860 1870 1880 1890 1900 1910 GGTCATCAGGCTGTCTCACTGCTAGCACCTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1920 1930 1940 1950 1960 1970 1980
TCCCGGTGGTAGAGGGAGGCCAGTGTGT-AGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGIGICTCGGGCCTCGGTGCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCTTCGCCCACGAAATCCG
                                                                                                                                                                                                                                                                                 ANACGCTTCTAGGGACAATAACCGATGAAAAAAAGATGGCCTCCTTGTGC-CCCCGTCTGTAATGATTTCTC
                                                                1900 1910 1920 1930 1940 1950 1960
GGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGCAGGAGGCTGAGAA
                              |||||| | AGGCAGTTATCTGATTAAAGAACACTAAAAGGCTAAAAGCCGCAGGATGTCTACACTATANCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 Significance = 117 Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                         US-09-030-606-110' (1-3410)
US-08-850-713-3 Sequence 3, Application US/08850713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Optimized Score = 102
Matches = 117
Conservative Substitutions
                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
43%
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       | | | | | |
GNACCNGGAGGA
500 510
                                                 80
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0 2080 x 2090 2100 2110 2120
GCTCGAGTGCCGAATCGCTGCACCAGCCGGTCCATGACCAGAGAAGACCAGGGA
                                                                                                                                                                                                                                                                                       GCCTTCATCAGCCCAGTCCTAGAGAGAGTAGAGGGGAGTGGAAGTGGGGGGGAACCAGGCTGGGCCAAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCATNACTCAGACTGGCCCGAAAAANCNCCCCAAAAACGGGNCCATGTCTTNNCGGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 600 610 620 520 --TTGGAATTATCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTT
                                                                                                                                                                                                                                                                                                                                                                                       990 300 310 320 320 350 360 ATACTCTGGGGGCTGAGATGGACAAAGGCTTGGGAAACCGCACTTTGTGTTCTGGTCCTGCAGTAGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 520 530 540 550 570. GAGGGGTGGTTAGGGAAGCCGTTG----AGACCTGAAGCCCCACCCTCTACCTTCAACACACCCTAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCNATNTNCATCACCTCCCGGGCNCANCAGGNCAAACCCAAAAAGTTCTTGNGGCCCNCAAAAAANCTCCGG 510 520 530 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGNCCCAGTTTCAACAAAGTCATCCCCCTTGGCCCCCAAATCCTCCCCCGNTTNCTGGGTTTGGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                          GGCAGGTTTATTGACAACCTCNCGGGACACAANCAGGCTGGGGACAGGACGGCAACAGGCTCCGGCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 160 170 180 190 210
TACAGTATAAAATTTCACCCCGCTAAATAAGACGACATTATTGCAAAGGGCACTTAAAACCCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 230 240 240 250 260 270 280 AGAGATAAGACTCCCCTTAGCTCAGGCAGGGGTGCTCCTGAGTTTCTGTGTGAGATTCCCCAAGCACAGAT
                                                                                                                                                                                                                          1.14
499
                                                                                                                                                                                                                        264 Significance 281 Mismatches
                                                                                                                                                                       )' (1-3410)
Sequence 32, Application US/08806596
                                                                                                                                                                                                                       Optimized Score = 264
Matches = 281
Conservative Substitutions
                                         90
                                                                                                                                                                   29. US-09-030-606-110'
US-08-806-596-32 Se
     2070
                    ACTGGCCAAATAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGTAACAGCAT---
                                                                                                                                                                                                                       Initial Score
Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370
                                                                                                       2130
GATGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440
      2060
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CACGCCTCTNNCTTTGGNNGGCAAGNTGGNTCCCCCTTCGGGCCCCCGGTGGGCCCNNCTCTAANGAAAACN
                                                                                                                                                                                                                                                                                             10 \qquad 20 \qquad 30 \quad x \qquad 40 \qquad 50 \qquad 60 \qquad 70
                                                                                                                                                                                                                                                                                                                  GTTGACAAGTTTCTTCTTCTAATCTTTTAAGGGGCGAGAAATGAGGAAAAAGAAAAGGATTACGCATA
390 400 410 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 160 170 180 190 200 · 210 TACAGTATAAAATAAGACGACATTATTGCAAAACGGCACTTAAAACCCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 650 660 670 680 690 710
TGGGGGGCCAGACCCCAGGAGAAGATTCTGGCAATGATCAGCCCAATGACCAGTATCTCAGGGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTTCATCAGCCCAGTCCTAGAGAGAGTAGAGGGGAGTGGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAACACAGAAAAGCTAGCAATGGATTCCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGATAAGACCTCCCTTAGCTCAGGCAGGGGGTGCTCCTGAGTTTCTGTGTGAGATTCCCCAAGCACAGAT
                                                                                                                                                                                                                                                 1.10
317
                                                                                                                                                                                                                                                  Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270
                                                                                                                                                                                                               )' (1-3410)
Sequence 105, Application US/09020747
                                                                                                                                   X 790 800 810 820 830 TACTTTGTTAAATAAATAAGTTAAATATTTAAATGCCTGTGTCTCTGTGAT
                                                                                                                                                                                                                                                 198
221
                                                                                                                                                                                                                                                                       Conservative Substitutions
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                                                                                                                                                                                                                                                  Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470
                                                                 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                  66
398
14
                                                                                                                                                                                                                US-09-030-606-110'
                                                                                                                                                                                                                                                  1 1 1
                                                                                                                                                                                                                                                  Score
Identity
                                                                                                                                                                                                                                                  Initial
Residue
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us-09-030-606-110-inv.res

580 % 590 600 610 620 630 TAACAGCATTTGGAATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGG             TGAAACCC X	US-09-030-606-110' (1-3410)  US-08-806-596-39 Sequence 39, Application US/08806596  ial Score = 66 Optimized Score = 228 Significance = 1.10  due Identity = 34% Matches = 478  10	150	### ##################################
580 x 590 TAACAGCATTIGGA 	31. US-09-030-606- US-08-806-596- Initial Score	150 16( TACAGTATAAAATATI	440  GTGCCTTCACAGG

590         600         610         620         630         640         650           720         730         740         750         770         780           TGTTGGGGATCCCCCACCTACCCAAATATTAGACACCAACACAGAAAAGCTAGCATTCCTTCTAC         1	750	S-09-030-606-110' (1-3410) S-08-904-809-39 Sequence 39, Application US/08904809  al Score = 66 Optimized Score = 228 Significance = 1.10  al Score = 66 Optimized Score = 267 Mismatches = 478  ue Identity = 34% Matches = 478  10	80 90 100 110 120 130 140  TTTTTTTTTTAAACATATAAGGCTTTAATTTTGTCACCATAAACATTATACTCTGATTGCTCACT	150 160 170 180  TACAGTATAAAATAAATAAATAAGACGACATTATTGCAAACGGCACTTAAACCCCCCCTG  TACAGTATTAAAATAATTCACCCGCTAAATAAATAAGACGACATTATTTTTTTT	220 230 230 240 250 250 250 270 270 270 270 270 270 270 270 250 270 270 270 270 270 270 270 270 270 27	90         310         320         330         340         350           ATACTCTGGGGCTGAGATGGACAAAGGCTTGGGACACTTTGTGCTTCTGGTCCTGCAGTGCTC           1   1   1   1   1   1   1   1   1   1	60         370         380         400         410         * 420         430           CAAACAGGGTGTGGGGGAAAGTTGGGGGAAATTTTGGGCA         1	440 450 460 470 480 490 500 GTGCCTTCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	510 520 530 540 550 560; 570  AAGAGGGGTGGTTAGGGAAGCCGTGAAGCCCCTCTACCTTCCAACACCCTAACCTTG
600 730 CCCCCACCTP       ACTNTCCTCNP 670 800 AAATAAGTTA	CTCCNCTNGTCCNNAATCNCCANC 730 740 750 60 CA	-606-110' (3-809-39 Sequents)  ity = 34' 0 20 TTTATTTTTT	90 ITTTAAACATA        TTTTTTAATGC	160 AAATATTCACC         TTTGTTTGCTC	230  ACCTCCCTTAC         TTTTCCTTTT	300 3GGCTGAG 	370 STTGTGGAGCT            CTTGTACAATT	40 45 ATCAGCCCAGI 1 1 1 NACCAACCCCN 390	520 TGGTTAGGGAA   GTTCTCATTNT
590 720 TGTTGGGGAT	CTCCNCTNGT 730 860 CA	32. US-09-030-US-08-904. Initial Score Residue Ident: Gaps  TTTTTTTT	80 TTTTTTTT         ATTTGATT 40	150 TACAGTATA               TTCATTTTA 100	220 AGAGATAAC       TGTGGCCT1 160	290 300 ATACTCTGGGGGCTG             GAAAAGGGGGTTTCG 230 240	360 CAAACAGGG I   ATTAACTGG	4 GTGCCTTC 11 CCTCCCCA	510 AAGAGGG   NGCNGAAN 450

33. US-09-030-606-110' (1-3410) US-09-020-747-39 Sequence 39, Application US/09020747

GTGCCTTCATCAGCCCAGTCCTAGAGAGAGTAGAGGGGAGTGGAAGTGGGGGGGAACCAGGCTGGGCCAAGAG

34. US-09-030-606-110' (1-3410) US-09-020-747-15 Sequence 15, Application US/09020747

Initial Score = 66 Optimized Score = 251 Significance = 1.10
Residue Identity = 36% Matches = 287 Mismatches = 482
Gaps = 26 Conservative Substitutions = 0

| SO | SO | 610 | 620 | 630 | 640 | 650 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 |

--GGTGCTCCTGAGTTCTGTGTGAGATTCCCCAAG

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	sccac   saaca	930 *: TTCTT      CTCTG 450 .	1000 TTTCATC         CTGGCAC 510	CAGGT   1   CACCC	111  11	1210 CCCTGT        ICCNNGG	80 SAGAGG			1.06 1019 0	10 20 X 30 40 50 . 60 70 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
	850 .ccaacag .1111 .gcaácaa	ACCTGG	10 AGTGTT   TTCTCT	1070 GGAAAC      TGACAA	1140 TGTTA?     NACAA!  650	CTGGCCTC CTGGCCTC CGAATCTN	1280 AGAGAGGAC			. 11 11 11	TTTTT	一ししいでする
	AAGGACC	920 3AGGGGA(   1   1 TTGANA!	990 TGGAGG CCANTG 500	1060 TAGAGATG            TNGAATTG	SGCTAGC	1200 CCTTC1 	X 1270 NGACTGGGG			Significance Mismatches	TTTTTT	
	840 AACAGA     NGGCTG( 360	910 GTGGGCTC        GTGGGCCC	ATCCCA'    CGCCAT	106( GGCTTAG2       TTCCTNG3	1130 TAGGAĞÜ 	OTGGAGC	X 1 ragaga( cccc		US/09020747		50 TTTTT	
	GATGGC       TATGGA	9] STGCTG1	980 STTCAAA SAAAGGG	1050 TTAAGG       NACANT 560	1120 GTCTCAAC       LAAATACNC 630	1190 AGTGCAT    AACTGCC	1260 2AGCCCJ       THCCCC		60/sn	461 494 tutions	TTTTT ,	- C
	830 CTCTGTC 11 1 TTCGTT	900 VAGACAC       SGGTGTC	970 GTCATATO 11 CTCCATGO	40 GCTGCAGG        GCTGCATC	112( GTGTGTCT TNAAAAA	1180 GCATTCC          IGCNTTTG	TCAGGC		Application	re = = Substi	40 TTTTTY	- 00
	20 CCTGTGT          CAAGAGT 340	GCAAAA TGTCNC	950 960 1000  CCTCAGGACTCTTCCCCTACAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATC	1040 CGAAGCT   1 111 SGCTGCT	1110 CTCTAG        CCCTGT	TCCCCG 	1250 CCTCCAGTG 	<b>.</b>	Applic	Optimized Score = 461 Matches = 494 Conservative Substitutions	TTTTT	— į
	820 AAATGCC 	890 GGATCA(       CTANCC'	960 CCTACA 11 CCCCCAG(	30 ATTAAA   1  ANCAAT	1100 CTCCCAAAACCCTTCTCT 	1170 GCAGAGT(      AAAGGGC)	1240 GGAAGGC I I I INAANCCC	10 SCTACG	10) e 109,	Optimized Matches Conservati	30 TTTTTT	, 1
	810 ATATTT GAGCAG	80 GGGGGGT 	9 CTTCCCC         ACTTTCCC	1030 AGCTACAT        CGCTGCAN	1100 CCAAAA         CCAACA	CT INTNAAC 680	CCCTTG	1310 GTGCAGC	(1-3410) Sequence 109,	318 N 365 O 36 C	20 X TTTTT	7
)	AGTTAA	880 TAAGAGGG 11111 GAAGAGTG 400	950 :AGGAC:      :ANGCG! 460	1020 ATGCAAG CCAGTTC	90 CAGCTC      ACCCTC	60 TCCAC-       TCCCCN	1230 GAAACCC( CCTGGTT(	1300 :ccc <b>A</b> GC:	5-110' 7-10 Se	ם נו נו	ATTTT	
)	800 TAAATA     TATGAC	870 !AAAAGG !CGGGAA	0             0	TCCCAT	1090 FTTATTCA CCCCCAAC	1160 3GGTAATC        CCNTTTTC 670	O CAGACT   NCCCCC 740	1 CAGCCC	30-606	Score Identity	10 PTTTT?	
	790         810         820         830         840         850           TTGTTAAATAATATATTAAATGCCTGTGTGTCTCTGTGATGGCAACAGAAGACCAACAAGGCCAC           1	CCTGAT   	940 950 1000 GTGTGTTGCCCTCAGGACTCTTCCCTACAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATC [	1010         1020         1030         1040         1050         1060         1070           CTAGAAACTCCCAGGTTAAGGGGCTTAGAGATGGGAAACCAGGT           I   I   I   I   I   I   I   I   I   I	1080         1100         1110         1120         1130         1140           GACTGAGTTATTCAGCTCCCAAAAACCCTTCTCTTCTGTGTGTG	1150 1160 1210 1200 1210  TGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTGT	1220	1290 1300 1310 GACGCCCCAGCTGTGCAGCTACGC	US-09-030-606-110' (1-3410) US-09-020-747-10 Sequence 1	al Scc lue Ide	TTTTT	
•	790 TTG7 11 CTG(	860 AT(   AC: 380	6T - 66	5-5	, ç <u>ç</u> ,	1. 1.027 1.026	A — A	G	35. U	Initial Residue Gaps	r	

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GGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCT
900 910 920 930 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 870 880 890 900 910 920
GCCCACATCCTGATAAAAGGTAAGGGGGGGGGGATCAGCAAAAAGACAGTGCTGTGGGGTGAGGGGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         930 940 950 960 970 980 990
GITCITGIGIGITGCCCTCAGGACICITCCCCTACAAATAAGICATATGITCAAATCCCATGGAGGAGTGT

        640
        650
        670
        680
        700

        TTTGGGGGGCCAGACACCCCAGGAAAGATTCTGGCAATGACCCAATGACCAGCTATCTCAGGGCAC
        TTTTGGGGGCCAATCTCCAGGGCAACGGGCAACGGGCAACTTCGGCAAAGTACAGGGCAACAGGGCAACTTCTACT
        TGCTGGTCAACTTGCTATTCTACTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACT
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                                                                                                 360 370 380 390 400 410 420
-AGTAGCTCCAAACAGGTTGTGGGGAAAGTTGGGGGAAAGTTGGGGGTAGGGGAAA
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 36. US-09-030-606-110' (1-3410) US-09-020-747-33 Sequence 33, Application US/09020747 Initial Score = 63 Optimized Score = 253 Significance = 0.98
Residue Identity = 35% Matches = 291 Mismatches = 502
Gaps = 33 Conservative Substitutions = 0

  7. US-09-030-606-110' (1-3410) US-08-806-596-2 Sequence 2, Application US/08806596 Initial Score = 62 Optimized Score = 266 Significance = 0.94
Residue Identity = 37% Matches = 312 Mismatches = 497
Gaps = 30 Conservative Substitutions = 0

420 430 440 450 460 470 480 490 and the same and the same

| 850 | 860 | 910 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920

8. US-09-030-606-110' (1-3410) US-09-020-747-2 Sequence 2, Application US/09020747 Initial Score = 62 Optimized Score = 266 Significance = 0.9 Residue Identity = 37% Matches = 49 Gaps = 30 Conservative Substitutions = 49

idue Identity = 3/\* Malcines

S Conservative Substitutions

400 410

350 360 370 380 390 400

CIGCAGTAGCTCCAAACAGGTTGTGGAGCTGGTGGGGAAAGTTGGGGGAAAGTTGGGGAAAGTTGGGGGAAAGTTGGGGGAAAGTTGGGGGAAAGTTGGGGGAAAGTTGGGGGAAAGTTGGGAAAGTTGGGAAAGTTGGGAAAGTTGGAAAAGTTGGAAAAGTTGGAAAATGTTGGATGGTGAAA

| 520 | 540 | 550 | 560 | 560 | 540 | 550 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560

| 850 | 860 | 870 | 880 | 900 | 910 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920

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530 540 550 560 --GAGACCTGAAGCCCCACCTTCTTCAACACCCTAA
                                                                                 GTCCAACCCCCTCNTCCAAATNNCCNTTTCCGGGNGGGGGTTCCAAACCCAANTTANNTTTGGANNTTAAAT
60 110 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 160 210 210 210 200 210 TACAGTATAAATAAATAAATAAAGACGACATTATTGCAAAACGGCACTTAAAACCCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAATNTTNNTTGGNGGNNNAANCCNAAT--GTNANGAAAGTTNAACCCANTATNANCTTNAATNCCTGGAA
0 140 150 160 160 170 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 230 240 250 260 270 280 AGAGATAAGACCTCCCTAAGGCAGGGGGGTGCTCCTGAGTTTCTGTGTGAGATTCCCCAAGCACAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTTNGAATTGGGANCCCNCGGGAATTAACGGGGNNNNTCCCTNTTGGGGGGCNGGNNCCCCCCCNTCG 410 420 430 440 450 460 460 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 450 460 470 500 500 GCCTTCATCAGCCCAGTCCTAGAGAGAGAGGGGAGTGGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAAA
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                                                                                                                                                                                                                                                                                     496
                                                                                                                                                                                                                                                                      216 Significance
246 Mismatches
                                                                                                                                                                                                                            )' (1-3410)
Sequence 20, Application US/08806596
                                                                                                                                                                                                                                                                                                 Conservative Substitutions
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32%
23
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US-08-806-596-20 Se
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TTTTTTTTTTTTTT
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580

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2640 2650 2660 2670 2680 2690 2700 AGGCATAGACAGAGTAGAGGCCTGGGGTCCGGGTCCGGGAAGAGGTCAGAGGCCTCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 720 730 740 780 750 770 780 CCTGATTGTTGGGAAAACCTAGCAATGGATTCCC
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X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctcagggacctcigactgctcigggccaagaarctcttgtttcttctactaggccaggcagcggtgartc 30 40 50 60 60 60 70 80 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCCCNTCCCTG-----GCTCTGANTCTCTGTCTTCCTGTCTGTGCANGCNCCTTGGATCTCAGT
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                                    NNTNGGGTTTNCCCCCCCCCANGGCCCCTCTCGNANAGTTGGGGGTTTTGGGGGGCCTGGGATTTTNTTTCCC 560 610 .
                                                                                             640 650 660 670 680 - 700 TITIGGGGGGGCCAGACCCCAGGAAGAAGAATTTGGCAATGACCAATGACCAGGTATCTAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2710 2720 2730 2740 2750 2760 ; 2770 GAGTGGAAGCACCCAGGAGCCCCAGGACCCCAGGATGAGCAGTGCCAGGTCCAGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCCTCNCTCANNGAACTCTGTTTCTGANNTCTTCANTTAACTNTGANTTTATNACCNANTGGNCTGTNCT 70 380 430 450 440
CCTTGGGTAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCCAAGGTCC'FGGG-----TTAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCCAGTGGTCACTGGCTGAGCCTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 Significance
273 Mismatches
                                                                                                                                                                                                                                                                  NTTNANTTAAATCCNTGCCTNGGCGAAGTCCNTTGNAGGGNTAAANGGCCCCCTNNCGGG
700 710 720 X
                                                                                                                                                                                                                                                                                                                                                                                                         40. US-09-030-606-110' (1-3410)
US-08-806-596-27 Sequence 27, Application US/08806596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative Substitutions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                                                TTCTACTTTGTTAAATAAATAAGTTAAATATTTAAATG
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31%
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score Residue Identity
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1060 1070 1080 1090 1100 1110 1120 TAGAGAACCAGGIGACTCTCAGGTGTCTCAACTAGG
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CATGGAGGAGTGTTCGTAGAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGTTAAGGGGCT
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US-08-904-809-19 Sequence 19, Application US/08904809
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Sequence 27, Application US/08904809
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US-08-904-809-27
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TGGCCTCCCTGTATAAGTCCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGG	1280 1390 1310 1320 1330  AGAGAGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCAGCACAGGGTGGCAGC	1340 1350 1360 1370 1380 1400 1410  AGAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCGGC	1420	1490 1500 1510 1520 1530 1540 1550 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAATGGCGACCAGACCCAGGCCTGCGGCAGACAC	1560 1570 1580 1600 1610 1620 CATATAGGCAGTGACAGTGGACCAGGACAGTGGGGGCCACCTGGGACAG CATATAGGCAGTGACAGACTGGACAGACATGGAGCCCATAAACAGGGGCCACCTGGGACAG	1630 1640 1650 1660 1670 1680 1690  CAGGAAGGCACTATCCAGGAGGTCCAGGCAGATGCCCCGGACCACCTGGCCTCGGTGGG  CAGGAAGCCACTATCCAGGATGCCAGGCAGATGCCCCGGAACCACCTGGCTGG	1700 1710 1720 1730 1740 1750 1760 1770 CTCACCCACCACCACCACCACGAGAGCCCCGCAGAGCGCGGGTGGGGGGGAGCAG  CTCACCCACCACCACGACGAGCATCACAGGCAGAGGCCCGCGGGTGGGGGGGG	X 1790 1810 1820 1830 GCCACTGCCTCCAGCACCCACGTGTCCATTAGGGAGGTCCAGGCTCCAGGCTTAGGGCTGG            NAATCCNCCT	43. US-09-030-606-110' (1-3410) US-08-806-596-18 Sequence 18, Application US/08806596	Initial Score = 59 Optimized Score = 259 Significance = 0.81 : Residue Identity = 34% Matches = 283 Mismatches = 507 Gaps = 19 Conservative Substitutions = 0	2160 2170 2180 2200 2210 2220 2230 ATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCTGGTACAGC

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CACTCATCATCACTGACTGAGGGACTTGGGCTCAGGATGTCCAGAGACGTGGTTCCGCCCCTCNCTT 450 460 470 480 510
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US-08-904-809-18 Sequence 18, Application US/08904809
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ACATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTT

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GGCCGGCGGCGCCATAGCGTCACTGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCC
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                                                               Significance
Mismatches
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Conservative Substitutions
US-09-030-606-110' (1-3410)
US-09-020-747-18 Sequence 18, Application
                                                                   Optimized Score
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19
                                                                              Initial Score
Residue Identity
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CGCCATGGCACTGCAGGGCATC X 10
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AGCCGGCGCAGCAGCAGCAGCAGCAGCCGGGGAAGCAGGCCCCAGGTTCCGG
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                                 TTGGTCCAAACCNTNCCNTGTGTCGANATNGTNAATCNGGNCCNATNCCANCCNCATANGAAGCCNG
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Mismatches
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Sequence 107, Application US/09020747
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Matches = 451
Conservative Substitutions
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US-09-020-747-10 S
          AGCACTGGACCAATGC
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660 710 , 720
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                                                                            CGGCCCTTGGGA---TGAGAAAGAGGCTCAGCAGGATG---CCCAAGGACAGTGCCCAGATGAAGGGCCGGC
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Mismatches
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Sequence 11, Application US/09525397
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Matches = 98
Conservative Substitutions
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US-09-525-397-11 St
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Gaps
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260 270 280 290 300 310 320 crccrgagtitctgtgtgtgttccccaagcacagatatactctgggggctgagatggacaaaggcttggga
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AACATCTTCCTGTATAATGCTGTAATATCGATCCGATNTTGTCTGCTGAGAATTCATTACTTGGAAAAGC 10 20 30 40
                                                                                                    620 630 640 650 660 670 680 GAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCCAGACCCCAGGAGAAGAAGATTCTGGCAATGATCA
                                                                                                                                                                          690 700 710 720 730 740 750 GCCCAATGACACCAATTAGACACCAA
                                                                                                                                                                                                                                                                                                                                                                                   40 550 560 570 580 590 600 610 ccccacccrctacctrcaccctaaccctrgggargacta
0.77
                                                                                                                                                                                                                                                                                                                          Significance
Mismatches
                                                                                                                                                                                                                                                                                            ' (1-3410)
Sequence 86, Application US/09020747
                                                                                                                                                                                                                                                                                                                           Optimized Score = 143
Matches = 163
Conservative Substitutions
                                                                                                                                                                                                          ccagcrccacaaccrgrrrggagcracrgcaggr
240 250 250 270 x
                                                                                                                                                                                                                                                                                            48. US-09-030-606-110'
US-09-020-747-86 Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
TTGCAAACGGCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||
|TTGATTCAACATCTT
||220 ||230
                                                                                                                                                                                                                                                                                                                            Initial Score Residue Identity = Gaps
                                                                                                                                                                                                                                                  760
CACAGAAAAGCTA
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Optimized.Score = 180
Matches = 195
Conservative Substitutions

58 40% 5

1 1

Initial Score Residue Identity

US-09-030-606-110' (1-3410) US-09-020-747-92 Sequence 92, Application US/09020747

470 480 AGGGGAGTGGAAGTGGGGGAAC ATACAGCCCANATCCCACCACG

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2890 2900 2910 2920 2930 2940 2950 TAGCGTCCACCCCAGTCACTGGCTAGGACCGGGACACAGA-CCAGGCCCAGCACTGGACCAAT:
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                                                                                                   GCCGCGACCGCATGTACGAGC X 10 20 3
                                                                                                                                                                                       CGTGACATACTGGAGATCGGGGCCCAATGGAGCATCCTACGCAANGACATCCCCTCCTTCGAGCGTACATG 170 180 230
                                                                                                                                                                                                                                  2600 2610 2620 2630 2640 2650 2660 AGGAGGTAGCCCAGGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCC
                                                                1100 3110 3120 3130 3140 3150 3160 CAGGCGCTCACCCACACCTTCAGGCCACTTCAGGCCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GGATGAAAATCGCNGGGTTGCTCCAGAAAGGCTN
550 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCTACCNCAAAGTNT
                                                                                                    2670 2680
GGGTCCCGGAAGAGGT
                                                                                                                        TAGTTCTTCTGGAGCT
                                                                                                                                                                                                                                 2820
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1180 1190 1200 1210 1220 1230 1240 CCCCGCATTCCAGTGCATGGAGCCCTTCTGGCTTCTGTATAAGTCCAGACTGAAACCCCTTGGAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACACTATAAACGTTAACGACCNAGATNANCACCTGCTTCA-----AGTGCAGGGAGGTACCTGACN 350 350 350 350
                                                                                                                                                  ANATTANTACAGTGTAATCTTT X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCTCCANCTGTGAAGGAAAAANNGATGGAATTTTNCCCTTCCGGCCNNTCCCCTCTTTGCACGC-C 520 530 530 540
                                                                                                                 820 830 840 850 860 870 890 CCTGTGTCTGTGTAAAAGGTAAGAGGGGGGTGGATC
                                                                                                                                                                                                                900 910 920 930 940 950. 960 AGCAAAAAGACAGTGCTGTGGGCTGAAGACCCTCAGGACTCTTCTTGTGTTGCCCTCAGGACTCTTCCCTACA
                                                                                                                                                                                                                                                                 TCCCAGAGGTGTGTANAGGGAACGGGCCTAGAGGCATCCCANAGATANCTTATANCAACAGTGCTTTGACC
                                                                                                                                                                                                                                                                                                                    970 980 1020 1030 AATAAGTCATAGATGTTCATCCTAGAAACTCCCATGCAAGAGCTACATT
                                                                                                                                                                                                                                                                                                                                                      AAACGAAGCTGCAG-GTTAAGGGGCTTAGAGATGGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1320 1330 1340 1350 1360 1370 1380 GCACCTCAGCAGCAGCAGCAGCAGCAGCAGAAACTGGCGGCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGTITICTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 1540 1550 1560 1570 1580 1590 1600 ACCAGACCCAGGCCTGCACACACACATAGAGCCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1110 1120 1130 1140 1150 1170 CCTTCTCTAGGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCC--TGGGTAATCCACCTGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Significance
Mismatches
(1-3410)
Sequence 26, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1290
                                               Optimized Score = 244
Matches = 290
Conservative Substitutions
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                                                                                                                                                                                                                                                                                                                                                                                                                        1060
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                                               34 & 28
                                                                                                                                                                                                                                                                                       40
US-09-030-606-110'
US-08-904-809-26 S
                                                  N D B
                                               Score
Identity
                                                               Residue
Gaps
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AATCAGCCAGGCGCCCATTICTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGC

3280

3270

3260

3250

3300

ACAGGGATTTCAGATGCTAAGG X 10 20

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1080 1090 1100 1110 1120 1130 1140 GACTGAGTTTATTCAGCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1440 1450 1460 1470 1480 1490 1500 GGCCTCCCACCCCAATGTGCGAAGTTTTCTACGTTGAGTATTTTGGCCAAGTCGTTTGTCAATACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTATGTGCCCCATCCTCCTTCATGCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACTTGTTTA
310 320 330 340 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1150 1160 1170 1180 1190 1200 1210 AGCCTGGGTAATCCAGTGCATGCAGTGCATGTGCAGCCCTTCTGGCCTCCCTGTATAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1610 1620 1630 1640 1650 1660 1670 AACAGGGATGGGGGCCACCTGGGACAGGAAGGCACTATCCAGGATGGCGAGGTCCAGGCAGATGCCCGG
                                                                                                                                                                                                                                                  0.73
                                                                                                                                                                                                                                                Optimized Score = 129 Significance
Matches = 140 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1510 X 1520 1530 1540 1550 1560 CTGTGTAGCAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACACATATAGG
                                                                                                                                                                                                            ' (1-3410)
Sequence 139, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         )' (1-3410)
Sequence 80, Application US/09020747
                                                                                                        CCNTNCCCCCCCNNNTCCTTTNCCC
800 810 820
                                                                                                                                                                                                                                                   57
368
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGCCTATCATCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53. US-09-030-606-1:
US-09-020-747-8
                                                                                                                                                                                                               52. US-09-030-606-11
US-09-020-747-13
                                                                                                                                                                                                                                          Initial Score Residue Identity Gaps
                                                                                                                                                                        CAG
```

Optimized Score = 152 Significance Matches = 168 Mismatches Conservative Substitutions

> 348 7

Initial Score = Residue Identity = Gaps =

```
1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --CCACTCAGTGGCAACACCCGGGAGCTGTTTTGTCGTTGTGGAGCCTCAGCAGTTCCCTCTTTCAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1490 1500 1510 1520 1530 x 1540 1550 AGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCAGGCCTGCGGCAGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCCAGGCGTCCCTCTGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1560 1570 1580 1590 1600 1610 1620 ATATAGGCAGTGACAGGCTGGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGC
                                                                                                                                                                      1490 1500 1510 1520 1530 1540 1550 GGCCAAGTCCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGA
                                                                                                                                                                                                                                                                                    1560 1570 1580 1590 1600 1610 1620 CACCATATAGGCAGTGACAGACTGGCTGGACAATGGAGCCCATAAAACAGGGATGGGGCCACCTGGGA
                                                                                                                                                                                                                                                        CAACTAGGAGGCTAGCTGTTAACCTGAGCCTGGGTAATCCACTGCAGAGGTCCCCGCATTCCAGTGCATGG
                            CCCCAGAGATCGTTTGAACCCTCTTATTTCAGAGGGGAAAATGGGGCCTAGAAGTTACAGAGCATCT
30 40
                                                                                        1200 1210 1220 1230 1240 1250 1260
AGCCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCGCAGCCTTAGA
                                                                                                                            0.73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Significance =
Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54. US-09-030-606-110' (1-3410)
US-09-020-747-11 Sequence 111, Application US/09020747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score = 427
Matches = 489
Conservative Substitutions
                                                                                      1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1670
                                                                                      1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1650
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378
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score = Residue Identity = Gaps = =
```

us-09-030-606-110-inv.re

rgaacaggagccaccargcagcrrcagcrrcarraagaccargargarccrcrrc 110 120 130 130 140 **\GGATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGCCTCGGTGGGC** AGGAAGGCACTATCCA CACTGCCAAGAGCCC

 1260

55. US-09-030-606-110' (1-3410) US-09-020-747-10 Sequence 100, Application US/09020747

0.69 172 0 Significance Mismatches Optimized Score = 97
Matches = 97
Conservative Substitutions 56 368 0 Initial Score Residue Identity Gaps

3390 GAGCCAGCG

GCCAGAAGGCTCCATGCACTG

CCAGTCAATGG----

Significance Mismatches

56. US-09-030-606-110 US-08-850-713-11

Initial Score = Residue Identity = Gaps =

```
1270 1280 1290 1300 1310 1320 1330 GAGACTGGGGGAGAGGAGGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1200 1210 1220 1230 1240 1250 1260 GGAGCCCTTCTGGCCTCCAGTCAGGCCTAAAGCCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1200 1210 1220 1230 1240 1250 1260 GGAGCCCTTCTGGCTCCAGTCAGCCCTA
                                                                                                                                                                                                                                                                                                                                         1270 1280 1290 1390 1300 1310 1320 1330
GAGACTGGGGAGAGAGAGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                       rccccacctacccaaatattagacaccaacacagaaaagctagcaatggattcccttctactttgttaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --AACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGG---
160 170 180 190 210 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGAAGGGTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTCAGCCCACAGCACTGTCTTTTGCTGATCCANCCCCCTCTTACTTTATCA 300 310 320 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59. US-09-030-606-110' (1-3410)
US-09-525-397-8 Sequence 8, Application US/09525397
                                                                                                                                      US-09-030-606-110' (1-3410)
US-09-071-710-8 Sequence 8, Application US/09071710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimized Score = 117
Matches = 133
Conservative Substitutions
                                                                                                                                                                                  Optimized Score = 117
Matches = 133
Conservative Substitutions
                1630 1640 1650
GACAGCAGGAAGGCACTAŢCCAGGATGGCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
368
23
                                                                                                                                                                                    56
368
23
                                                                            800 810 TAAATATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCATCAGCCCAGTCCTAGAGAGAGTAGAGGGGAGTGGGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAAGCCTTCACAAGTTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 520 530 540 550 550 570 GGGTGGTTAGGGAAGCCGTTGAAGCTTGAAGCCTTGGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600 610 620 630 640 650 CATTIGGGAIGAATITCCAAGGICCIGGGITAGGCAITTIGGGGGGGCCAGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660 670 680 690 700 710 720 CCCCAGGAGAAGAAGATTCTGGCCAATGACCCAATGACCAGCTATCTCAGGGGACCTGATTGTTGGGGA
                                                                                                                                                                                                                                                                                                                            CTCTATTGCTACTATTAAAAAAAATCACAAATCTTTCCCTTTAAGCTATGTTNAA
0 120 130 160
                                                                                                                                                                                                    2510 2520 2530 2540 2550 2560 2570 GAAGATGAGGGGGCCAGGGCACTGGTGCTCCTGGGTGCCCAGGTAGGGGGCCCAGGGCACTGGTGTC
                                                                                                             GTGTTGGTGTCTAATATTTGGG
                                                                                                                                                                                                                                      2590 2610 2610 2620 2630 2640 ----CAGGCAGGAGGTAGCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Optimized Score = 95 Significance Matches = 100 Mismatches Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )' (1-3410)
Sequence 133, Application US/09020747
                  Application US/08850713
   ' (1-3410)
Seguence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 56
. 35%
                                                 56
40%
10
```

57. US-09-030-606-11 US-09-020-747-13

2790 GCACAGCAGCCCT

Initial Score = Residue Identity = Gaps

GCCAGAAGGCTCCATGCACTG X

CAATTTGTGGAACAACA

730

CAGCATTTGGAATTAT

```
63.
          GCAGCAGAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGGCTAACA;
                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAGAAGGGTCCATGCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 1490 1500 1510 1520 1530 1540 1550 TTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCCTGCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGG
                                                               1210 1220 1230 1240 1250 1260 CCCTGTATAAGTCCAGACCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GATTTGAACATATGAAAGTTATTTGTAGGGAAGAGTCCTGAGGGGCAACACAAGAACCAGGTC 230 230 240 250 260 270 280
                                                                                                                                                                                                   1560 1570 1580 1590 1600 X 1610 1620 GACACCATATAGGCAGTGACAGGCTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGG
                                                                                                                                                                                                                                                                                                                                                    0.69 \\
209
                                                                                                                                                                                                                                                                                                                                                      . . .
                      Optimized Score = 117 Significance Matches = 133 Mismatches Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0' (1-3410)
Sequence 8, Application US/09841894A
                                                                                                                                                                                                                                                                                                                                                  Optimized Score
Matches
                                                                                                                                                                                                                                                                       1630 1640 1650 GACAGCAGGAAGGCAGG
                                                                                                                                                                                                                                                                                                                                                  56
368
23
                                                                                                                                                                                                                                                                                                                 60. US-09-030-606-11
US-09-841-894A-8
                                                                                                                                          TTGGCCAAGTCGCTCT
                                                                                                                                                                                                                                                                                                                                                                                              1200
GGAGCCTTCTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GATTTGAAC
                                                                                                                                                                                                                                                                                                                                              Initial Score
Residue Identity -
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1420
                                                                                                                                  1490
1340
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X 10 20
TTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AANAFGGTAGCTTTCANAFGTNCCCTCAGTCCCAATGTTGCTCAGATAAATAAATCTCGTGAGAACTTACCA
270 - 280 330
                                                                                                                                                                                                                                                                                                                        AGAAAGCCTTTAATTTTGTCACCATAAACATTATACTCTGATTGCTCACTTACAGTATAAAATATTCACCCC
                                                                                                                                                                              AANATGGTAGCTTTCANATGTNCCCTCAGTCCCAATGTTGCTCAGATAAATAAATCTCGTGAGAACTTACCA 270 320 330
                                                                                                                                                                                                                                 · 100 110 120 120 130 140 150 160 AGAAAGCCTTTAATACTCTGATTGCTCCCCTTTACTTACAGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.65
                                                                                       0.65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.65 \\ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Significance
Mismatches
                                                                                       Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                            170 x 180 190 200 210 220 GCTAAATAAAAAGACGCACTTAAAACCCCCCTGAGAGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )' (1-3410)
Sequence 103, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )' (1-3410)
Sequence 52, Application US/09020747
                                                               US/08904809
                                                                                      Optimized Score = 72
Matches = 72
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 72
Matches = 72
Conservative Substitutions
                                                 61. US-09-030-606-110' (1-3410)
US-08-904-809-52 Sequence 52, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score
Matches
1630 1640 1650 GACAGCAGGAGGACTATCCAGGATGGCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55
418
0
                                                                                       55
418
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55
36%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-030-606-110' US-09-020-747-10 Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-030-606-110'
US-09-020-747-52 S
                                                                                          0 8 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 0
                                                                                      initial Score
Residue Identity
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score
Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTCTTGT
490
                                                                                                                                                                                                                                                                                                                                                                                                                   CACTCTTGT
490
```

1320 1330 134  ACCTCAGCAGCACAGGGTGGCAGC		1680 1690 170 CGGAACCAGGGA-ACGGAACCAGGGA-ACGGAACCACCTGGCCTCGGTGGAACCACCTGGCCTGG	1,300   1,00	TATTTGGGCAGGAACACCTGCTGTGTGTGTGTGTGTGTGT	670 680 2030 2040 X GGCAGCCACAGGGAAAGCTGCCA                   AGNCCCACNGGANANNCG 740 750	65. US-09-030-606-110' (1-3 US-09-020-747-12 Sequer Initial Score = 55 Residue Identity = 34% Gans
Gaps = 28 Conservative Substitutions = 0  10 20 30 40 50 60 70  TITITITITITITITITITITITITITITITITITIT	150	290 310 320 330 340 350 360  ATACTCTGGGGGCTGAGATGGAAAAGGCTTGGGAAACCGCACTTGTGTCTTCTGGTCCTGCAGTAGCTCCA	330 340 350 360 370 380 390  440 450 460 470 480 490 500  GCCTTCATCATCATCTAGAGAGAGAGAGAGAGAAGAGA	460 470 480 490 500 510 520 530 580 590 600 610 620 x 640 TAACAGCATITGGAATTAGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTGGGGGGCC 1111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AGACCCCAGGAGAAGATTCTGGCAAT  64. US-09-030-606-110' (1-3410)  US-08-904-809-12 Sequence 12, Application US/08904809  Initial Score = 55 Optimized Score = 243 Significance = 0.65  Residue Identity = 36% Matches = 280 Mismatches = 465  Cans = 16 Conservative Substitutions = 0	1250 1260 1270 12 CTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAG

```
| 1990 | 2000 | 2010 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 2020 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1910 1920 1930 1940 1950
CITCICCCGGIGGIAGAGGCCAGIGIGIAGGGCAGGAICIGCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACACTTGAGTGAAGTCTTCTGGGAACCATAATCTTGTTGATGGCAGG 260 270 280 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1560 1570 1580 1590 1600 ACCATATAGGCAGTGACTAGACTGGCTGAGTGACATAAA
rcattggcrgrg--rrggrgacgrrgrcarrgcacacacagaargggggaaa
120 150 130 140 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.65
479
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 Significance = 267 Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -3410)
ence 12, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 Optimized Score = 243
34% Matches = 267
20 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score
Residue Identity
Gaps
```

 CA

66. US-09-030-606-110' (1-3410) US-08-806-596-10 Sequence 10, Application US/08806596 Initial Score = 55 Optimized Score = 271 Significance = 0.65
Residue Identity = 38% Matches = 319 Mismatches = 464
Gaps = 36 Conservative Substitutions = 0

n

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Н

Thu May

```
10 2220 2230 2240 2250 2260 2270 228U TCTGGGCACGCCCTGGTACACCCCTCGCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCAT

        2640
        2650
        2660
        2670
        2680
        2690
        2700

        TAGACAGAGAGGACAGAGCAGAAGAGGCCTCCAGTGGAGTG

                                                                               1860 1870 1880 1890 1900 1910 1920 CTGTCCTCACTGCTGCTCCCGGTGGTAGTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAG
                                                                                                                                                                                                                                                                                                                                                     CAGTCTAINTGGCCAGTGTGGC x 20
                                                                                                                                                                                                                                                                                                                                                                                             1930 1940 1950 1960 1970 1980 1990 AGGGAGGCCAGGTGTGT-AGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGCGGCGGCGGCTGAAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                       2290 2300 2310 2320 2330 2350 CCAGCTGCACAGCTCAGCACCACCAGCAGCCGCCGGCGCGGGGGCATGCGGCAGCAGCTGGTGCAGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2360 2370 . 2380 2390 2400 2410 2420 GGGGAAAGCAAGGAAAGCCAAGGCGCCCGGCATGGACAGGGGCGACAAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TTTATGGGCTCCATGTCCAGCTCAGCCAGT
                                                                                                                                                                                                                                                              0.65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2490
                                                                                                                                                                                                                                                             271 Significance
319 Mismatches
                                                                                                                                2710 X 2720 2730 2740 2750 2760 AAGCACCTGGCCACAGAAGTCCAGGAGCCCACAGGATGAGCAGTGCCA
                                                                                                                                                                                                                         (1-3410)
Sequence 10, Application US/08904809
                                                                                                                                                                                                                                                             Optimized Score = 271
Matches = 319
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2180
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36*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2440
                                                                                                                                                                                                                       67. US-09-030-606-11
US-08-904-809-10
                                                                             2080
                                                                                                                                                                                                                                                             Initial Score = Residue Identity =
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        TAGACAGAGTAGGCCTGGGTCCCGGAAGAGGTCAGAGGGCCTCCAGTGGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTGTTCCTG-CCCAAATACCGAGGGACACTGGAGGTGCTAGCAGGACAGCCTGATGACCAGCTTC

170 180 200 210 220 230
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                                                                                                                                                                                                                                                                                                                                                                                                                             ACTGGGTCCAACTCCCCGCTCCTGTTAACCCCATGGGGCTGCCGGCTTGGCGGCGCCAATTCTGTTGCTGCCAA 650 650 650 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1860 1870 1880 1890 1900 1910 1920 CTGTCCTCACTGCTCCCCGGTGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1930 1940 1950 1960 1970 1980 1990 AGGGAGGCCAGTGTGT-AGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTGT
                                                                                                                                                         CAGTCTATNTGGCCAGTGTGGC
                                            2570 2580 2590 2600 2600 2610 2620 2630 AGGGCACTGGTGTCCCAGTGATGAGGCAAAGGCAAAGGCAAGGCAAGGTGATGAAGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 271 Significance Matches = 319 Mismatches. Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68. US-09-030-606-110' (1-3410)
US-09-020-747-10 Sequence 10, Application US/09020747
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Residue Identity =
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700 710 720 730 740 750 760 TEST TATCTCAGGGGACCTGGTTGGGGATCCCCCACCCTACCAAATATTAGACACCAAAAAGCTAG
                                                                                                                                                              ) 2590 2600 2610 2620 2630 2630 AGTCAATGGCAGGCAGGTAGCCCAGGCAGCCCCCAAGACTGATGAAGGCA
                                                                                                                                                                                                                                                                                                                                                        GCCCCAATTCCAGCTGCCACAC X
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                                                                                                                                                                                                                                                                                                                                                                                                                                       630 640 650 660 670 x 680 690 CTGGGTTAGGCCATTTTGGGGGGCCCAGACAGAGAAGAATTCTGGCAATGATCAGCCCAATGACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGANGCCAGGGTGCTTCCGGGGCCGGGGCATC----TGCCTGGACCTCGCCATCCTGGATAGTGCTTCTT
380 420 430 440 440
                                                                                                                     ---TTTATGGGCTCCATTGTCCAGCTCAGCCAGT 470 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAATGGATTCCCTTCTACTTTGTTAAATAAGTTAAATATTTTAAATGCCTGTGTCTCTGTGATGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GTGACGTTGTCATTGCAAC
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )' (1-3410)
Sequence 16, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Optimized Score = 262
Matches = 317
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGTCCCANGTGGCCCCATCCCTG---
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US-08-904-809-16
                                                                                                                                                                                                                                                          GCAGGTGAGGAAGATG
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Residue Identity -
Gaps -
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1060 1070 1080 1090 1100 1110 1120 TAGAGATGGGAAACCAGGTGACTGTTATTCAGCTCCCAAAAAACCCTTCTCTAGGTGTGTCTCAACTAGG
                                                                                                                                                                                                                                                                                                                                                                                                    CGCCNGCTGCGAATGAAAANTACCCACGTTGACAAACTGCATGGCCACTGGACGACAGTTGGCCCGAAN
80 490 500 510 510 550
                                                                                                                                                                                                                  GGCTCTTGGCAGTGAATTCTGANAAAAGGAACNGCNTNAGCCCCCCCAAANGANAAAAACACCCCGGGTGT 700 740 750 750 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1200 1210 1220 1230 1240 1250 1260 GCCCTTCGGCCTCCAGTCAGGCCCTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 920 930 940 940 950 960 970 980 CTGAGGGGACCTGGTTCTTCCCCTACAAATAAGTCATATGTTCAAATCC
                                            ----ACACTIGAGIGAAGICTICCIGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGAGAGCCACATTA-----CTTTGGCAGCAACAGAAACTGGCGGCCAGCC.GGCAGCCCATGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.65
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70. US-09-030-606-110' (1-3410)
US-09-020-747-11 Sequence 110, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 426
Matches = 522
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2270
                               AGCACTTGAGCCCTTTCATGGTGGTGTTCC--
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42%
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Residue Identity
Gaps
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GACACTATGATGAAGGCGTTCGG 1230 1240 71. US-09-030-606-110' (1-3410) US-09-020-747-14 Sequence 149, Application US/09020747 Initial Score = 54 Optimized Score = 76 Significance = 0.61
Residue Identity = 38% Matches = 81 Mismatches = 126
Gaps = 1 Conservative Substitutions = 0

1060 1070 GCTTAGAGATGGGAAACCAG 72. US-09-030-606-110' (1-3410) US-09-071-710-4 Sequence 4, Application US/09071710

Initial Score = 54 Optimized Score = 93 Significance = 0.6 Residue Identity = 42% Matches = 110 Mismatches = 13 Gaps = 9 Conservative Substitutions = (

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1580 1590 1600 1610 1620 1630 1640 GCTGAGCTGGACAATGGAGCCCCATAAACAGGGATGGGGCCACCTGGGACAGGAAGGCACTATCCAGGAT
                                                                                                                                                                                                                                         1580 1590 1600 1610 1620 1630 1640 GCTGAGCTGGGACAGCAGCACCTATCCAGGAT
                                                                                                                                                                                                                1800 1810 1820 1830 1840 1850 1860 GTGTCCATTAGGGAAGCTCCACGCTTAGGGCAGGCAGGAAGCTGGTCATCAGGCTGTCACTCCTCACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1800 1810 1820 1830 1840 1850 1860 GTGTCCATTAGGGAGGTCCAGGCTTAGGGCTGTCCTCACTGCT
                                   GCTCCCTTCCCTAATGGACACG
                                                                                                                                                                    GGAGACATCACAGGCCAGAGGCCCCGCAGAGCGCGGGTGGAGGTGGGAGCAGGCCACTGCCTCCAGCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1870 1880 X 1890 1900 1910 1920 1930 AGCACCTCCAGTGTCCCCGTGGTAGAGGCCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGGGGGCCAA
                                                                                                                                                                                                                                                                                      Optimized Score = 93 Significance Matches = 110 Mismatches Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                      0' (1-3410)
Sequence 4, Application US/09525397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1770
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230 240 X
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                                                                                                                                                                                                                                                                                                                                                                      73. US-09-030-606-11
US-09-525-397-4
                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score
Residue Identity -
Gaps
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Application US/08850713

74. US-09-030-606-110' (1-3410) US-08-850-713-5 Sequence 5,

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GCTCCCTTCCCTAATGGACACG
                                                                                                                                          1800 1810 1820 1830 1840 1850 1860 GIGTCCATTAGGGAAGGGAAGGCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCTCACTGCT
                                                                                                                                                                                                                                                                                                                                                 TCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCTGTTTATGGGCT---CCATTGTCC 170 180 190 200 210 2210 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCCCTTCCCTAATGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1580 1590 1600 1610 1620 1630 1640 GCTGAGCACAGCAGCACCACTATCCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1580 1590 1600 1610 1620 1630 1640 È GCTGAGCTGGACAATGGACCCATAAACAGGATGGGGCCACCTGGGACAGCAGGAAGGCACTATCCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1730 1740 1750 1760 1770 1780 1790 GGAGACATCACAGGCCAGAGCCCACCCAGCACCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1800 1810 1820 1830 1840 1850 1860 GIGTCCATTAGGGAAGGGAAGGGAGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCTCACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCT---CCATTGTCC 170 210 220
                                                                                                                                                                                                                                                                                                                                                                                                    1870 1880 X 1890 1900 1910 1920 1930 AGCACCTCCAGTGTCCCCTCGGTAGAGGGAGGCCA
Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75. US-09-030-606-110' (1-3410)
US-09-841-894A-4 Sequence 4, Application US/09841894A
 Optimized Score = 93
Matches = 110
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 93
Matches = 110
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
428
9
  54
428
9
                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score = Residue Identity = Gaps =
 Initial Score
Residue Identity
Gaps
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370 380 390 400 410 AGGGTTGTGGGGGAAAGTTGGGGGTAGGGG ACAGAAATGTTGGATGGTGGAG X Significance Mismatches Substitutions )' (1-3410) equence 2, Application Optimized Score Matches Conservative Suk 54 378 30 76. US-09-030-606-110' US-08-904-809-2 Se 420 430 AAATTTTGGGCAGTGCC CTGCAGTAGCTCCAAAC Initial Score = Residue Identity = Gaps

GAAACCAGGTGACTGAGTTTATTCAGCTCCC-----AAAAACCCTTCTTAGGTGTGTCTCAACTAGGAGG TCGTGCCACTGCNTTANTGAATCNGCCACCCCCGGGAAAAGGCGGGTTGCNTTTTGGGCCTCTTCCGCTTTC

GAG

US-09-030-606-110' (1-3410) US-09-071-710-16 Sequence 16, Application US/09071710 77.

0.61 1294 0 Significance Mismatches Optimized Score = 704 Matches = 838 Conservative Substitutions 54 378 89 11 11 initial Score Residue Identity = Gaps

CAGCAGAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC -TAACA

TTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCA ATGGACACGTGGGTGCTGGAGGCAGTGGCCTG--440 450

 | 2910 | 2910 | 2920 | 2930 | 2940 | 2950 | 2950 | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 | 2970 |

3260 3270 TTCTGCCAGCCCTTTGG

Initial Score = 54 Optimized Score = 704 Significance = 0.61
Residue Identity = 37% Matches = 838 Mismatches = 1294
Gaps = 89 Conservative Substitutions = 0

   3260 3270 TTCTGCCAGCCCTTTGG 79. US-09-030-606-110' (1-3410) US-09-841-894A-1 Sequence 16, Application US/09841894A Initial Score = 54 Optimized Score = 704 Significance = 0.61
Residue Identity = 37% Matches = 838 Mismatches = 1294
Gaps = 89 Conservative Substitutions = 0

  1980

1970

2040 2050 CACAGGGAAAGCTGCC

CTTCCAAGGGGGTTTC 1000

2180

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CAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGT-----GCCACATGCCTGTCCCACAGTG 230 170 180 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200 1210 1220 1230 1240 1250 1260 gagcccttctggcctccctgtataagtccagactgaaaccccttggaaggcctccagtcaggcagcctaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .050 1060 1070 1080 1090 1100 1110
TAAGGGGCTTAGAGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTAGGTGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         980 1040 1010 1020 1030 1040 1040 TTCAAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 3200 3210 3220 3230 3240 .13250
GGCTCTGCTGCTGCTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCAT
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4. US-09-020-747-17 Sequence 174, Application 1169 790 1112

5. US-09-020-747-17 Sequence 174, Application 1119 482 597

6. US-09-020-747-17 Sequence 177, Application 1119 482 597

7. US-09-020-747-45 Sequence 45, Application 234 155 204

7. US-09-020-747-45 Sequence 45, Application 234 155 204

8. US-08-806-596-23 Sequence 23, Application 801 872 93 240

9. US-08-806-596-16 Sequence 109, Application 801 84 268

10. US-08-904-809-16 Sequence 16, Application 801 84 268

11. US-08-904-809-8 Sequence 8, Application 05 799 76 252

14. US-09-020-747-13 Sequence 69, Application 536 69 185

15. US-09-020-747-69 Sequence 69, Application 799 76 252

16. US-09-020-747-13 Sequence 3, Application 05 773 65 263

19. US-09-020-747-3 Sequence 3, Application 05 773 65 263

19. US-09-020-747-3 Sequence 3, Application 05 773 65 263

19. US-08-904-809-3 Sequence 3, Application 05 773 65 263

19. US-08-0020-747-3 Sequence 3, Application 05 773 65 263

19. US-08-904-809-3 Sequence 3, Application 05 773 65 263

19. US-08-904-809-3 Sequence 3, Application 05 773 65 263
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Application 1167 790 1
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Application 1248 803
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Total Elapsed 00:00:01.00
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                                                                                                                                                                                                       The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-020-747-17 Sequence 173, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110, Application 36, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-020-747-17 Sequence 171, **** 11 standard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The list of other best scores is:
 CPU
00:00:01.00
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Sequence

Standard Deviation 63.84

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Scores

Thu May

	19.27	
747	1265 Significance = 19.27 1265 Mismatches = 0 utions = 0	
JS/09020	1265 1265 tutions	i
ication [	score = = = re Substif	
65) ce 173, Appl	1265 Optimized Score = 1265 100% Matches = 1265 0 Conservative Substitutions	
3 (1-12 Sequen	1265 100% 0	
1. US-09-030-606-173 (1-1265) US-09-020-747-17 Sequence 173, Application US/09020747	ial Score = due Identity =	
÷	Init Resi Gaps	

 2. US-09-030-606-173 (1-1265) US-09-020-747-17 Sequence 171, Application US/09020747 Initial Score = 803 Optimized Score = 1130 Significance = 12.03
Residue Identity = 91% Matches = 1163 Mismatches = 19
Gaps = 95 Conservative Substitutions = 0

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C CNTC	1070 119 ACCT 	1260 AAA2             AAA2	ni es	Gaps GGC <i>I</i>	0700 	AGTC   AGTC	220 AACI 	290 CGG2 CGG3	1939 1939 1939	CAG!	101 111
220 230 240 250 260 270 280 250 260 270 320 ATCAAGTIGGACGAATCCGAGTCTGACACCATCCGGAGCATCGCATTGCTTCGCAGTGCCTACC	ATCAAGTTGGAGTTCTGAGTTCTGACTACC         290       30       310       350       360         390       370       380       390         GCGGGGAACTCTTGCCTCGTTTCTGGCTGGGGTCTGCTGCGGTGTGTCTGCCC       111111111111111111111111111111111111	400 410 420 430 440 450 460 TCTTCAAGGAGGTCCTCTGCCGGGGGGGTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCG	470       480       490       500       510       530         TGCTGCAGTGAGGTGTCTGCAGTAAGCTCTATGACCCGCTGTACCACC         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	540         550         560           CCAGCATGTTCTGCGCGGGGCCCCTGA           CCAGCATGTTCTGCGCGGGGCCCCTGA           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	610         620         630         640         650         670         680           TCTGCAACGGGTACTTGCAGGGCCTTGTGTTTTTTTTTT	690         700         710         720         730         740         750           TCTACACCTCTGCAAATTCACTGAGATAGAGAAACCGTCCAGGCCAGTTAACTCTGGGGACTGG           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	760         770         780         790         810         820           GAACCCATGAGAATTCAGGAATTCAGGAATACCTCCTC	830   840   850   860   870   880   890   CCTCAGGCCCAGGAGCCCCCAGCCCCTCCTCCTCCTCCTCCAAACCAAGGGTACAGATCCCCAGCCCCTCCTCTTTTTTTT	900 910 920 930 940 950 960  CCCTCAGACCCAGGACCCCCAGCCCTCCTCAGACCCAGGAGTCCAGCCCTCCTCCTTC	970         980         1000         1010         1020         1040           AGACCCAGGCCCCCAGCCCCCCCCCCCCCCCCCCCCCC	1050 1060 1010 1080 1090 1110  TTCAGAGTCAGAGCCCCAACCCCTGTTCCCCAGACCCAGAGGTNNAGGTCCCAGCCCTCTTC

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11.83
30
0
                                                     1 1 1
                                                     Significance
Mismatches
                                                US/09020747
                                                     ore = 1112 :
= 1137 P
Substitutions
                                               Application
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Matches
Conservative
                            175,
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Sequence 1
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83
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410 420 430 440 450 460 470 480	580         600         610         620         630         640           ACTCTGCAACGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAA           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	720 GATAGAGA           GATAGAGA	740 780 780 780 770 780 770 780 770 780 770 780 770 780 770 780 770 780 770 780 770 780 770 780 770 780 770 780 770 780 78	800         810         850         860           GAATTCAGGAATATCTGTTCCCAGCCCTCCTCCTCCTCCTCCTCGGAGTCCAGGCCCCCAGCCCTCCTCCT         111111111111111111111111111111111111	870   880   990   910   920   930   930   TCAAACCAAGGGTACAGGCCCCTCCTC   1111111111111111111111111111	940 950 1000  CCTCAGACCCAGGAGTCCAGCCCTCCTCCNTCAGACCCAGGAGTCCAGACCCCAGCCCTCCTCCTCA	1010 1020 1030 1040 1050 1060 1070 1080  GACCCAGGGGTTGAGGCCCCCAACCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCCTTCGTTCCC	1090 1110 1110 1120 1130 1140 1150 1150	1160 1170 1180 1200 1200 1210 1220 GNACACAGTGCCCCTTGTGGNANGTTGACCCAACCTTACCAGTTGGTTTTTTTTTT	1230 1240 1250 x TAGATCCAGAAATAAGTTTAAGAGANGNGCAAAAAAAAA	4. US-09-030-606-173 (1-1265) US-09-020-747-17 Sequence 174, Application US/09020747	Initial Score = 529 Optimized Score = 688 Significance = 7.74 Residue Identity = 59% Matches = 710 Mismatches = 454 Gaps = 31 Conservative Substitutions = 0	50 60 70 80 90 X 100 110 GGAAAACGAATTGTTCTGCTCGGGGGGGTGCTGCATCCGCACTGTTTCCA

us-09-030-606-173.res

10.00   10.0
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TCACTTGGCCTCAACCATCTTGGTATCCAGTTATCCTGAATTGAGATTTCCTGCTTCAGTGTCAGCCAAGCCA 650 650 650 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790 800 810 820 830 840 850 GGAAGGAATTCAGGAATTCCCAGCCCCACCCTCAGGCCCCAGGCCCCAGCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTATCATGATTACTGTTGACTGTGTCTATTGTACTAACCATGCCGATGTTTAGGTGAAATTAGCG 570 580 590 600 610 620 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCCCAGACCCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCACTAGATTT
--TTGCCATCCAGTCCCAGACTGTGGGAGGCTTGGGAGTGTGAGAAGCTTT 380 410
                                                                                                                                                                                                                      650 660 670 - 680 690 7.00 710 CGGAAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCACCTCTGCAAATTCACTGAGTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                  720 730 740 750 760 780 AGAGAAACCGTCCAGGCCAGTTAACTCTGGGGACCGGAACCCATGAAATTGACCACAAATACATCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                   940 950 960 970 980 980 1000 TCCTCCCTCAGACCCCAGAGCCCCCAGGCCCTCCTC
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30 1060 1070 1080 1090 1100 1110 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1150 1160 1170 1180 1190 TCCCTGNACACAGTGCCCCTTGTGGNANGTTGACCCAACCTTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1080
 GCGAACGATGCTGTGA---
360 370
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1.88 0 0

Significance Mismatches

Optimized Score = 204 Matches = 234 Conservative Substitutions

Initial Score = Residue Identity = Gaps

0 Q

6. US-09-030-606-173 (1-1265) US-08-904-809-45 Sequence 45, Application US/08904809

240 25 CGACCTCATGCTC [	170 180 200 210 x 220 230 530 530 530 530 600 530 600 530 600 600 600 600 600 600 600 600 600 6	250 260 270 280 300 300 300 CTCATCAGATTGCTTC 8. (CTCATCAAGATCGTGTCGAGACTCGGAGCATCGGATTGCTTC 8. (CTCATCAAGATCGGTCGAGATCTGACACCATCGGAGCATCGGATTGCTTC 8. (CTCATCAAGTTGGACGATCGTGTCGAGATCGGAGCATCGGAGCATCGGAGCATCGGAGCATCGGAGCATCGGAGCATCGGAGCATCGGAGCATCGGAGCATCGGAATCGGTCGAGACCATCGGAGCATCGTTTCTGGCTGG	### ### ##############################	-030-606-173 (1-1265) -020-747-45 Sequence 45, Application US/09020747 Score = 155 Optimized Score = 204 Significance = 1.88 Identity = 73% Matches = 0 Identity = 73% Matches = 0 Identity = 73% Matches = 0 Identity = 190 x 220 230 Igentity = 190 x 220 230 Igentity = 190 x 200 210 x 220 230 Image: 180 x 20 x		100 110 420 430 880 880 890 890 890 890 890 890 890 89
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| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 
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1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 | 1020 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     680 720 730 730 730 730 GIGCCAGGIGTAGAGAAAACCGTCCAGGCCA
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GGGCCCCTGATCTGCAGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAACCANGCNGGCGAATCGTAATNAGGCGTGCGCC-----GCCAATNTGTCNCCGTTT
0 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 470 480 490 500 510
ATGCCTACCGTGCTGCGTGTCGGTGTCTGAGGAGGTCTGCAGTAAGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCAAACTATACTTCGCTCGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 330 340 350 x 360 370
TGCCCTACGGGGGAACTCTTGCTTGCTGGGGTCTGGTGAACGGTGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 Significance = 276 Mismatches =
                                                                                       540 550 560 570 580
ACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506-173 (1-1265)
596-23 Sequence 23, Application US/08806596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 Optimized Score = 240
30% Matches = 276
30 Conservative Substitutions
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ity =
             170
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GNCNCCCTCTTTCC 860 870 X 9. US-09-030-606-173 (1-1265) US-09-020-747-10 Sequence 109, Application US/09020747 Initial Score = 89 Optimized Score = 444 Significance = 0.85
Residue Identity = 388 Matches = 495 Mismatches = 753
Gaps = 30 Conservative Substitutions = 0

X 10 20 GGCAGCCCGCACCCT

(1-1265) Sequence 16, Application US/08806596 10. US-09-030-606-173 US-08-806-596-16

0.77 474 0 gnificance Optimized Score = 268
Matches = 320
Conservative Substitutions 84 398 25 Initial Score Residue Identity Gaps

GCCCCAATTCCAGCTGCCACAC X 10 20 220 2 GTACAACAGACCCTTG

| 580 | 590 | 600 | 610 | 620 | 630 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640

US-09-030-606-173 (1-1265) US-08-904-809-16 Sequence 16, Application US/08904809 11.

0.77 474 0 Significance Mismatches Optimized Score = 268
Matches = 320
Conservative Substitutions Optimized Score 39% 25 K & 6 Initial Score
Residue Identity a

550 520

us-09-030-606-173.res

TGCGGAAGGAATTCAGGAATATCTGTTCCCAGCCCCTCCTCCTCCAGGCCCAGGAGTCCAGGCCCCCAGGCC ---TGGCCCGAANATCTTCAGAAAAGGGATGCCCCATCGATTGAAC TGCATGGCCACTGGACGACAGT----

Sequence 16, Application US/09020747 (1-1265)12. US-09-030-606-17; US-09-020-747-16

0.77 474 0. Significance Mismatches Optimized Score = 268
Matches = 320
Conservative Substitutions 398 25 Initial Score Residue Identity Gaps

GAGGAGGTCTGCAGTAAGCTCTATGACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGGCAAGAC 510

720 730 740 750 , o o caragada a contra a contra

| 940 | 950 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990 | 990

US-09-030-606-173 (1-1265) US-08-904-809-8 Sequence 8, Application US/08904809

Significance - Mismatches -Optimized Score - 252
Matches - 281
Conservative Substitutions 76 34% 22 Initial Score Residue Identity Gaps

 500
 510
 520
 530
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 CTGAGGAGGTCTGCAGTAGCCGGCTGTACCAGCCCAGCATGTTCTGCGCCGGCGGAGGGCAAG
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570         580         600         610         620         630           ACCAGAAGGACTCCTGCAACGGGTACTTGCAACGGGTACTTGCAGGGCCTTGTGT         1
610 620 630  TGATCTGCAACGGGTACTTGCAGGGCCTTC
610 SCCCTGATCTG           SCCTTGCTGCCC
600 ACTCTGGGGGG       SANCCGCTCTG
590 rgcaacgerga   1
580 SAAGGACTCC1 
570 ACCA(

  14. US-09-030-606-173 (1-1265) US-09-020-747-13 Sequence 136, Application US/09020747 Initial Score = 70 Optimized Score = 130 Significance = 0.55 Residue Identity = 34% Matches = 140 Mismatches = 257 Gaps = 4 Conservative Substitutions = 0

5. US-09-030-606-173 (1-1265) US-08-904-809-69 Sequence 69, Application US/08904809 Initial Score = 69 Optimized Score = 185 Significance = 0.53
Residue Identity = 37% Matches = 204 Mismatches = 328
Gaps = 9 Conservative Substitutions = 0

 CGTTGGGGGGGTGAATTACTTCTTCGACGTAGAGGTGGGCCGAACCATATGTACCA 330 350 GAGCCAGGCAACAGAC 310

**ACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATG** 450

16. US-09-030-606-173 US-09-020-747-69

Optimized Score = 185 Significance Matches = 204 Mismatches Conservative Substitutions Sequence 69, Application US/09020747 69 378 9 Initial Score Residue Identity Gaps

AGGTCCTCTGCCCAGTCGCGGGGGTGACCCAGAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGT 440

GGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCA

17. US-09-030-606-173 (1-1265) US-09-020-747-40 Sequence 40, Application US/09020747

0.50 462 0 Optimized Score = 249 Significance Matches = 279 Mismatches Conservative Substitutions 67 36**%** 30 Initial Score Residue Identity Gaps

GTGGTATTTCTGTAAGATCAG 

TCTGCAACGGTGACTCTGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTTTCGGAAAA GCCACCAGGAACTICTCAAAGTICCAGGCAACNICGTIGCGACACACCGGAGACCAGGTGAINAGCTIGGG

680 670

CCCTCCTCCTCCAAACCAAGGGTACAGATCCCCAGCCCTCCTCCTCAGACCCAGGAGTCCAGACCCCCA

### GATTTC

# 3. US-09-030-606-173 (1-1265) US-09-020-747-3 Sequence 3, Application US/09020747

Initial Score = 65 Optimized Score = 263 Significance = 0.47 Residue Identity = 36% Matches = 290 Mismatches = 481 Gaps = 22 Conservative Substitutions = 0

950
GAGTCCAGCCCTCCNTCAGACCCAG

20. US-09-030-606-173 (1-1265) US-08-904-809-32 Sequence 32, Application US/08904809

Initial Score = 65 Optimized Score = 255 Significance = 0.47
Residue Identity = 35% Matches = 289 Mismatches = 499
Gaps = 35 Conservative Substitutions = 0

650

900

590

| 810 | 820 | 830 | 840 | 850 | 860, | 870 | 840 | 850 | 860, | 870 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 84

| 880 | 890 | 900 | 910 | 920 | 930 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940

 1090 11100 1110 1120 1130 1140 1150 1160 aggregation of the control of the contro

21. US-09-030-606-173 (1-1265) US-09-020-747-84 Sequence 84, Application US/09020747 Initial Score = 64 Optimized Score = 125 Significance = 0.45
Residue Identity = 39% Matches = 135 Mismatches = 201
Gaps = 8 Conservative Substitutions = 0

22. US-09-030-606-173 (1-1265) US-09-020-747-21 Sequence 21, Application US/09020747

Initial Score = 63 Optimized Score = 209 Significance = 0.44
Residue Identity = 32% Matches = 250 Mismatches = 500
Gaps = 31 Conservative Substitutions = 0

| 550 | 560 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610 | 610

1260 AAAAAAAA . US-09-030-606-173 (1-1265) US-08-806-596-38 Sequence 38, Application US/08806596

Initial Score = 62 Optimized Score = 208 Significance = 0.42 Residue Identity = 32% Matches = 245 Mismatches = 479 Gaps = 31 Conservative Substitutions = 0.42

1250 GANGNGCAAAAAAAA | | CCCGGGNCGGCCG 720 X 24. US-09-030-606-173 (1-1265) US-09-020-747-11 Sequence 110, Application US/09020747 Initial Score - 62 Optimized Score - 437 Significance - 0.42
Residue Identity - 37% Matches - 481 Mismatches - 766
Gaps - 37 Conservative Substitutions - 0

310 320 330 340 350 360 370 CGCAGTGCCTACCTGCTTCTGCCTGGGGTCTGCTGGCGAACGCTCACGG CGCAGCGTCACGG CGCAGCGTCACGG CGCAGCGTCACGG CGCAGCTCACGG CGCTCACGG CGCTCAGGCCTCAGGCCTCAGGCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCTCAGGCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCTCAGGCCAGGCCTCAGGC

TNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCACCTAGATTTTCCCTGNACACAGTG  AAGGCGTTCGGATGGGCTGTTCCTGCAGTGCGCCATCTCCTGGTCTTCTCTCTGTCATGG  40 1250 1260 1270 1280 1290 1330  1170 1180 1200 1200 1210  CCCCCTTGTGGNANGTTGACCTTACCAGTTGGTTTTTCATTTTTNGTCCCTTTCCCCTAG  CCCCCTTGTGGNANGTTGACCCAACCTTACCAGTTGGTTTTTCATTTTTNGTCCCTTTCCCCTAG  ACCGGCTGGTGCAGCCACTCGAGCAGTTTTTTGGCCAGTTTTCCCTTTCCCTTTCCCTTTCCCTTTCCCTTTCCCTTTCCCTTTCCCTTTCCCTTTCCCTTTCCCTTTCCTTTCCTCT	230 1240 1250 X ATCCAGAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	173 (1-1265)  36 Sequence 36, Application US/08904809  60 Optimized Score = 253 Significance = 0.39  348 Matches = 283 Mismatches = 516  20 Conservative Substitutions = 0	TTCTGCTCGGGCGTC	110 120 130 140 150 160 170  TGTTTCCAGAACTCCTACACCATGGGCTGGGCCTGCACAGGCCGAGCCAGGGAGCCAG  I	180 190 200 210 220 230 240  ATGGTGGAGGCCACCTACGGCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACCTCATG  1	250 310 310 CTCATCAGAGTCCGAGTCTGACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCT CTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCT	20       330       340       390         ACCGCGGGGAACTCTTGCCTCGCTGGCGTCTGCCGACGGTCACGGGTCTCTCTG       1       1         1   1   1   1   1   1   1   1   1   1	400 410 420 430 440 450 460 460	470
CAGCCCTCTTCC 	1240 TAAAGITTAAGAGAI 	(1-12 Sequen 60 34%	50 SGAAAACGAATTGTT	120 GAACTCCTACACCAI              TGACNAAGGCTCCCT	190 200 GGCCAGCCTCTCCG1          AACCAGTAAGCCTGC	260 2: CTTGGACGAATCCG:            CCTGTAGGAAAGCC	330 340 igaactcttgcctcg     iaaaaaaaaaataaa 250 26	400 CCAGGAGGTCCTCTG                CTCACTTCTGCTTGG	70 TGCAGTGCGTG L
TNNAGGTCC	1230 1240 ATCCAGAAATAAAGTT	25. US-09-030-606-173 US-08-904-809-36 Initial Score	caps 40 CTGGTCATC	110 TGTTTCCA(        CGTTTCCA(	180. ATGGTGGA      ATCATACN 100	250 CTCATCAA       20 110	320 ACGCGGG             ACTAATGC	CCCTCTTC 1 1 1 1 1 CCCAGCGC 310	47( CCGTGCT(         CNTTTCC)

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CICATCAAGTIĞĞACGAATCCGIGICCGAGICIGACATCCGGAGCATCAGCATIGCIICGCAGIGCCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 120 130 140 150 160 170 TGTTTCCAGAACTCCTACACCATCGGGCCGACCAGGGAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 190 200 210 220 230 240
ATGGTGGAGGCCAGCTACGGCACCAGAGTACAACAGACCTTGCTCGCTAACGACCTCATG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGNCGCTTTCNGCCGCCCCX
                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 750 | 760 | 770 | 780 | 790 | 800 | 810 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 
                                                                                                                                                                                                                                                                                                                                     CINGAACCATGGTGCCCTTCCGGTCTGATCCNAAAGGAATGTTCCTGGGTCCCANTCCCTCTTTGTTNCTT 630 640 650
                                                                                                                                                                                                                                                                          680 690 700 710 720 730 740 GIGCCAGIGIAGAGAAAACCGICCAGGITAACIC
                                                                                                                                                      600 610 620 630 640 650 650 670 GGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.39
516
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Significance = Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      890 x 900 910 920 930 940 TCCCCAGCCCCTCCTCAGACCCC
AAGTCTCNGCCCACAAGACCGGCCACCAGGGGANGTCNTTTNCAGTGGATCTGC--
460 470 480 490 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-1265)
Sequence 36, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Optimized Score = 253
Matches = 283
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
348
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-030-606-173
US-09-020-747-36 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 11 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGAAAAACCACNCN
810 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial Score Residue Identity Gaps
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	470	530         540         550         570         580         590           CTGTACCACCCAGCATGTTCTGCGCGGCGGGGGCAAGACCAAGGGACTCCTGCAACGGTGACTCTGGG         1	0   610   620   630   640   650   670   670   660   670   660   670   660   670   660   670   660   670   660   670   660   670   660   670   660   670   660   670   660   670	680         690         700         710         720         730         740           GTGCCAGGTGTACACCTCCAGGCCAGTTAACTC         I	750 760 70 730 790 800 810 TGGGGACTGGGAACCCATGAATTGACCCCCAAATACATCCTGCGGAAGGAATTCAGGAATATCTGT	820   830   840   850   860   870   880   1000   880   1000   880   1000   880   1000   880   1000   880   1000	B90 x 900 910 920 930 940 TCCCCAGCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC	(1-1265) Sequence 160, Application US/09020747	59 Optimized Score = 126 Significance = 0.38 38% Matches = 148 Mismatches = 219 15 Conservative Substitutions = 0	X     10     20     30     40     50     60     70       GGCAGCCCGCACTGCACTGGTCATGGAAAACGAATTGTTCTGCTCGGGCGTCCTG     1 </td <td>  80   90   100   110   120   130   GTGCATCC GCAGTGGGTGGGCC   CACTGTTTCCAGAACTCCTACACCATCGGCTGGGCC   130   1</td> <td>0 150 160 170 180 200 TGCACAGTCTTGAGGCCGACCAGGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACG  </td> <td>230 240 250 260 270 .</td>	80   90   100   110   120   130   GTGCATCC GCAGTGGGTGGGCC   CACTGTTTCCAGAACTCCTACACCATCGGCTGGGCC   130   1	0 150 160 170 180 200 TGCACAGTCTTGAGGCCGACCAGGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACG	230 240 250 260 270 .
CTTCTGCT	TGCGTG 1 	40 CAGCATGT'   1	CTGCAACG	CTACACCAN	760 PACCCATG, 111111 GACCCNTG	830 CCTCCCTCA(           TCTGCCCTA(	X 900 TCCTCCT   NCN X	)-606-173 ( )-747-16 Se		CTCGCAGC	90 AGTGGGTG           AGACAGAG	16 GGGTCTGA( 1 1 1 1 1 GGGTCTGA(	220
	470 CCGTGCTGCAGTGCGTG 	530 CTGTACCACCC          AAGTCTCNGCC 460	600 GGGCCCCTGAT [11 11 ANTACCCNTAT 520	680 GTGCCAGGTGT 	750 TGGGGACTGGG 1 ACTTGTNTTG 660	820 TCCCAGCCCT     TTCNTAAATTC 730 74	B90 X TCCCCAGCCCTCCY         NGAAAAACCACNCN 810 X	27. US-09-030-6 US-09-020-7	Initial Score Residue Identity Gaps	x 10 GGCAGCCGCA       ACCTGCAT	80 GTGCATCC-GC             ATACTTCCAGG	140 TGCACAGTCTTT           TGANAATGTG	210

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Gregrarrirereradarea
x 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 590 600 610 620 630 640 650 TCCTGCAACGGTGATTTCGGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 740 750 760 770 770
ACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAA-----ATACAT
            650 670 680 690 720 720 690 700 720 720 GCCCCGTGCGAAGTTGGCGTGCCAGGTGTCTACACCACCTCTGCAAATTCACTGAGTGGATAGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACCCAGAGTACAACAGACCCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGA
                                                                                                                                350 360 370 x 380 390 400 410 CTGGGGTCTGCTGCCTCTTCAAGGAGGTCTTGCCCAGTC
                                                                                                                                                                                                                                                                                                                                     300 310 320 340 350 360 360 340 350 360 360 360 GAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGAACTCTTGCCTTGGCTGGGGTCTGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                         370 380 390 400 410 420 430 GAACGGTGAGGTCTCTCTCTCTCTCTCTCTCTCCCAGTCGCGGGGCTGACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCTCTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGTGTCTGAGGAGGTC
                                                                                                                                                                                                                                                                                      0.38
462
0
                                                                                                                                                                                                                                                                                      249 Significance
279 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490
                                                                                                                                                                                                                                                    28. US-09-030-606-173 (1-1265)
US-08-904-809-40 Sequence 40, Application US/08904809
                                                                                                                                                                                                                                                                                                             Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                       1 1
                                                                                                                                                                                                                                                                                                                                    330
                                                                                                                                                                                                                                                                                      Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460
                                                                                                                                                                  CGAAACTTGTAGAATGAAGCCTGGA 350
                                                                                                                                                                                                                                                                                     368
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450
                                                                                                                                                                                                                                                                                         1 1 1
                                                                                                                                                                                                                                                                                     Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                     420
GCG
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840 850 860 870 880 890 900 GGAGCCCCTCCTCAAACCAAGGGTACAGATCCCCAGCCCCTCCTCAGACCC AAGAGCTGCGCACATTCCTGCAGAAAAGGTGGCGGTCCCCATCACTCCTCTCCCATAGCCATCCC 110 120 140 150 150 160 AGAGGGTGAGTAGCCATCANGCCTTCGGTGGGAGGGAGTCANGGAAACAACANACACACAGAGCANACAGAC 170 180 190 230 700 720 750 760 -TCTGCAAATTCACTGAGTGGATAGAGAAACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAA ANATTANTACAGTGTAATCTTT X 10 1080 1090 1100 1110 1120 1130 1140 CCTCGTTCCCAGACCCAGAGGTNAAGGTCCCAGCCCTCTTCCNTCAGACCCAGAGGTCCAATGCCACTA 50 560 570 580 590 600 610 620 GCCCGGCCGGCGCAACACGGTGACTCTGGGGGCCCCCTGATCTGCAACGGGT NTGGTTCCTCTCAAGGANCCCATATCTCNACCANTACTCACCNTNCCCCCCCNTGNNACCCANCCTTCTAN 630 640 650 930 940 950 960 970 980 990 eccentrated and contradate and contrad TTCCTTGANGGAATTCCCAAATCTCTTCGNTCTTGGGCTTCT-NCTGATGCCCTANCTGGTTGCCCNGNATG 450 450 510 Optimized Score = 197 Significance = 204 Mismatches = Conservative Substitutions = = (1-1265) Sequence 26, Application\_US/08806596 CTATCTGNACCCCNCNTTGTCTCANTNT 730 740 750 X 59 30% 2 29. US-09-030-606-173 US-08-806-596-26 S Initial Score Residue Identity GATTTTC 550 Gaps

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1060 1070 1080 1090 1100 1110 1120
TCCAAGCCCCCAACCCTGGTTCCCCAGAGGTNNAGGTCCCAGGCCCTCTTCCNTCAGACCCAGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 1140 1150 1160 1170 1180 1190
GTCCAATGCCACCTAGATTTTCCCTGNACACAGTGCCCCCTTGTGGNANGTTGACCCAACCTTACCAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITATGTGGTTTTTATATATAAGATGCACTTTATGTCATTTTTTAATAAAGTCTGAAGATTAC 300 240 240 250 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAGAGACTGTCGCTTCCTCCGTTGTTGCGTGAGAACCCGTGTGCC----CCTTCCACATATC

30 40 50 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       920 930 940 950 960 970 980 AGTCCAGGCCCCCCCAGGCCCCAGGAGTCCAGGCCCTCCTCCATCAGACCCAGGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGCCTTTCCCTCAGAATTCAG
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 850 860 870 880 890 900 910 GICCAGGCCCTCAGACCAAGGGTACAGATCCCCAGCCCTCTCCTCAGACCCAGG
                                                                                                                                                                                                                                                                                       GTGAAGGAAAANNGATGGAATTTTNCCCTTCCGGCCNNTCCCCTCT-TCCTTTACACGCCCCTNNTACTC 530 540 550 550
                                                                                                                                                                                                                                                                                                                                                                                                                                       NTCTCCCTCTNTTNTCCTGNCNCACTTTTNACCCCNNNATTCCCTTNATTGATCGGANNCTNGANATTCCA
                                  CNNNAACTGCNGCCTGGGGACAGCNCTGGGANCAGCTAACNNAGCACTGCCCCCCTGCCCCCCATGGCCGTNCG
390 400 410 420 430 430
                                                                                                                     1060 1070 1080 1090 1100 1110, 1120
AGGTCCAAAGCCCCCAAACCCTCGTTCCCCAGACCTNNAGGTCCCAGCCCTCTTCCNTCAGACCCA
                                                                                                                                                                                  CNTCCCTGGTCCTGNCAAGGAAGCTCCCTGTTGGAATTNCGGGGANACCAAGGGANCCCCCTCCTCANCT
460 470 480 490 500 510
                                                                                                                                                                                                                                               1130 1140 1150 1160 1170 1180 1190
GNGGTCCAATGCCACCTAGATTTTCCCTGNACACAGTGCCCCCTTGTGGNANGTTGACCCAACCTTACCAGT
990 1000 1010 1020 1030 1040 1050
TCCAGACCCCCCAGCCCTCCTCAGACCCAGGGGTTGAGGCCCCCCAACCCCTCCTTCAGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                        Significance = Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 x 1210 1220 1230 1240 1250
THITTCATTITHGECCTTTCCCCTAGATCCAGAAATAAAGTTTAAGAGANGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-030-606-173 (1-1265)
US-08-904-809-66 Sequence 66, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CINNCGCCTNCCNTCNATCNGNAANACNAAANACTNTCTNACCCNGG 670 690 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
41%
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 N N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial Score
Residue Identity
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	Application
	99
31. US-09-030-606-173 (1-1265)	1S-09-020-747-66 Segmence
	_

0.36 174 0 Significance Mismatches Substitutions 115 131 Optimized Score Matches Conservative Suh Initial Score Residue Identity Gaps

910 890 840

TTTTTCATTTTNGTCCCTTTCCCCTAGATCCAGAAATAAAGTTTAAGAGANGNG 1200 x 1210 | ||| TGTTT

## Sequence 17, Application US/08806596 (1-1265)32. US-09-030-606-173 US-08-806-596-17 £

0.34 .442 0 Significance Mismatches Optimized Score = 250
Matches = 289
Conservative Substitutions 38 38 29 Initial Score Residue Identity Gaps

| || || || ---rescaacaccessacrerariers GTGAGAGCCACCCTCTGCCTGCCACTCAG-X 10 30

TACAACAGACCCTTGCTCGCTAACGACCTCATGCTCAAGTTGGACGAATCCGTGTCCGAGTCTGACACC

470

790 800 CTGCGGAAGGAATTCAGGA

Sequence 17, Application US/08904809 (1-1265)US-09-030-606-173 US-08-904-809-17 8 33.

0.34 442 0 Significance Mismatches 250 289 Conservative Substitutions Optimized Score Matches 57 38% 29 0 11 11 Initial Score Residue Identity = Gaps

CACAGTCTTGAGGCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCT.CGTACGGCACCCAGAG

| 360 | 370 | 380 | 390 | 410 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420

790 800 CTGCGGAAGGAATTCAGGA 34. US-09-030-606-173 (1-1265) US-09-020-747-17 Sequence 17, Application US/09020747

Initial Score = 57 Optimized Score = 250 Significance = 0.34 Residue Identity = 38% Matches = 289 Mismatches = 442 Gaps = 29 Conservative Substitutions = 0

| 80 | 90 | 100 | 110 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |

| S80 | 590 | 600 | 610 | 620 | 630 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620 | 620

| 650 | 660 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710

790 800

35. US-09-030-606-173 (1-1265) US-09-020-747-11 Sequence 111, Application US/09020747

Initial Score = 57 Optimized Score = 429 Significance = 0.34
Residue Identity = 36% Matches = 783
Gaps = 44 Conservative Substitutions

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130	210 :GGCACCCAG         :TGTTGCCAG 200		350 3GCTGGGGTC          CCTGGGCTG	420 GTCGCGGGGC                 ATCTTCATTGC	) rggrgrcrga         rgcrggragr	570 GCAAGACCA.               GAAAGGGCT 560	640 FTGTGTCTTT        STGCCTTTCC .630	710 STGAGTGGAT      STCACGACCA 700	780 TACATCCTGC 1 11 GTGGTGTGGC	30 840 -AGGCCCAGGAGT 	900 CCCTCAGACC         AGCAGTGATT 920	) IGACCCAGGA 111 IGACTTGGGG 990
120	0         150         160         170         180         190         200         210           TGCACAGTCTTTGAGCCAGGGAGCCAGGCCAGGCCTCTCGGTACGCACCCAGGGACCCAGGGACCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGAGCAGAGCCAGTTGAGAGCATAAAGACCATGATGAGACCATGATGCAGAGCCTGTTGCAGAGCCTGTTGCAGAGCCTGTTGCAGAGCCTGTTGCAGAGCCAGATGGCAGAGCCAGATGGCAGAGCCAGATGGCAGAGCCTGTTGCAGAGCCAGATGCAGAGCCAGATTAAAAAAAA	220 230 240 250 260 270 280 AGTACAACAGACCTTGCTCGAACGAATCCGTGTCCGAGTCTGACA	290 300 310 320 330 340 350 CCATCCGGAGAGCATCAGCCTTGCCTTGCCTGGGTGCTGGGTGCTGGGTGCTGGGTGCTTGCTTTGCTTTGGCTGGGTGTGTGTGTGTGTTGT	360   370   380   390   410   420	430         440         450         470         480         490           TGACCCAGAGCTCCCAGGCAGAATGCCTACCGTGCTGCAGTGCGTGTCGGTGGTGTCTGGTGTTCTTGGTGTTCTTGGTGTTGT	0         510         520         530         540         550         560         570           GGAGGTCTGCAGCTGTACCCCCCCCCCCCCCCCCCCCCC	580 590 600 610 620 630 640  GAAGGACTCCTGCAACGGTGACTTGCAGGGCCTTGTGTTTTTTTT	650         670         680         690         700         710           CGGAAAAGCCCCGTGTGGCCAAGTTGCCAAGTTGCCAAGTTCACTGAGTGGAT         1<	720         730         740         750         760         770         780           AGAGAAAACGTCCAGGCAGTTAACTCTGGGGACTGGGAACTCCCAAATTGACATCCTGC         1	790         800         810         840           GGAAGGAATTCAGGAATATCTGTTCCCAGCCCTCCTCCTCCTCCTCCTCCTCCTCCAGGAGT         1         <	850   860   870   880   890   900   900   CCAGCCCCCCAGCCCCTCCTCAAACCAAGGTACAGATCCCCAGCCCTCCTCCTCAGACC   1   1   1   1   1   1   1   1   1	910         920         930         940         950         960         970           CAGGAGICCAGACCCAGGACCCAGGAGICCAGGACCCAGGA         1
110	190 GGAGGCCAGG      CTTTCTGTG1	260 GTTGGACGAA        CTTCGGGCCA	330 GAACTCTTGC           GTGGTCTTTC	CAAGGAGGTCC CAAGGAGGTCC 	480 SCAGTGCGTGAN SGCTGAGCACT	550 ATGTTCTGCC       CAAGTGTGGA	620 :AACGGGTAC: 	690 PACCAACCTCT         WACCTGCACCA	CCATGAAATTC	ATGTATCTG1	ACAGATCCCA ACAGATCCCA           GAAGAGGCACC	)
100	180 GCCAGATGGT       ATTTGCTCAI	250 TGCTCATCAA           TTCTGAAGAT	320 CTACCGCGG       AGCCGGCGTT	CTGCCCTCTTCA CTGCCCTCTTCA CTGTGACGTTCT B0 390	470 TACCGTGCTG( 111 CACCACAATG(	540 CCACCCAGC          AGACTTCACT	610 CCTGATCTGC       TGAGGACTC?	680 AGGTGTCTAC   1 AGCCAATGAA	750 GACTGGGAACC ATGACATCCGA	TCCTCCCTC -	870 8 AACCAAGGTA 1 11 TGGGAACTGTG	950 AGACCCAGGA( 
06	170 SAGCCAGGGA       ATCCTCTTCA	240 AACGACCTCA       3GGCCATCCT 230	310 rcgcagrecc 	380 39 GGGTGTGTCT        AAGTGTGCCCTC	460 SCAGAATGCC'         CCTTGGTGTA(	530 ACCCGCTGTA           STTCCCAGGA	600 CTGGGGGCCC       ATACGGATTT 590	670 TTGGGTGCC I I I TCACCAACAC	740 7 TAACTCTGGGG               CAGCTTTTGTA	820 rcccagcccc;             rgcrcccar	860 8 TCCTCCCTCAA               TGCTGCCACAT 880	940 STCCTCCTCA         ATGTCACTTG
80	160 GCCGACCAA(    ACCATGATG/ 150	230 TTGCTCGCT/             TCAATCGAT(	300 AGCATTGCT           GGCTACT	GAGCTCACGG L   1 CTGAGAGCAA	450 GCGTCCCAG       CTGTGGTCG	520 AGCTCTATGA          AAGATTATG(	590 ACGGTGACT(   111 TCACCAACT/ 580	660 GTGGCCAAG'          ATGACAACG'	0 AGGCCAGTI       GCTTCAATC	810 AATATCTGT   GCCTCGAGC	CCAGCCCTCTCTCTCGCCCTCTCTCTCTCTCTCTCTCTCT	930 ccccagccc l l garcraaca
70	150 CAGTCTTGAG         CTTCATTAAG	220 CAACAGACCC 	CCGGAGCATC CCGGAGCATC   1   1 TGTCAACGTG	0 370 GGCGAACGGTGJ        GGTGCTAAGACJ	440 CCAGAGCTCT 1 GTTGCAGCTG 430	510 GTCTGCAGTA           GCCATCAAGA 500	580 GACTCCTGCA 11 11 TGCTGTGGCT 570	650 AAAGCCCCGT TTCTGTTGCA	0 730 AAAACCGTCCA(       GTAGAGGGTTG( 720	10   800   810   820	850 GGCCCCC TTCTGCCTCTG	920 AGTCCAGACC GAGGGGACAG 930
	140 TGCA(   TCAG(	AGTA(   TGGG( 2.	CCATO	360 TGCTG 11 CTATG 350	430 TGACC         TGAGC	500 GGAGG 1 GCCTG	GAAG	CGGA 	720 AGAGA     AAAAG' 710	790 GGAA(     AGCT( 780	CCA III CCAC	910 CAGG       GGGGG

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CCCACTCAGTGGCAACACCGGGGAGCTGTTTGTCCTTTGTGGANCCTCAGCAGTN:CCTCTTTCAGAACTC 30 40 50 50 60 70 80 90
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Matches = 281 Mismatches
Conservative Substitutions
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US-08-806-596-13 Sequence 13, Application US/08806596
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CCCACTCAGTGGCAACACCGGGGGGGTGTTTTGTGTGGGANCCTCAGCAGTNCCCTCTTTCAGAACTC 30 40 50 60 70 80
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GGCGGAAGGCCAAGGACTCCTGCAACGGTGACTCTGGGGGGGCCCCTGA
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Mismatches
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Sequence 13, Application US/08904809
360
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Matches = 281
Conservative Substitutions
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CTCCCTCAGACCCAGGACCCCCCAGCCCTCCTCCT
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16
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US-08-904-809-13
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400 410 420 430 4440 450 460 TCTTCAAGAGGTCCTCCAGGCAGAATGCCTACCG
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TCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCCGTGTGGCCAAGTTGGCGTGCCAGGTG
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Mismatches
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US-09-020-747-13 Sequence 13, Application US/09020747
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Matches = 281
Conservative Substitutions
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CICCCICAGACCCAGGAGCCCCCAAGCCCTCCCT
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38%
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NTGGTTCCTCTCAAGGGANCCCATATCTCNACCANTACTCACCNTNCCCCCCCNTGNNACCCANCCTTCTAN 590 600 610 620 630 640 650

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      670
      680
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      GCCCCGTGTGGCCAGGTGTCTACACCTCTGCAAATTCACTGAGTGGATAGAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 410 420 430 440 440 450 470 A70 A70 AAGAAGTCCTGCCCAGGCGGGGGTGCCTGCCTGCGTGCTG
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580 590 600 610 620 630 640 650 TCCTGCAACGGTGCTTGCAGGGCCTTGTTGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGACCNCTCANCCGGNCNNNCNACCNCCGGCCNATCANNGTNAGNNCACTNCNNTTNNATCACNCCCCNCC 30 40 50 60 70 80 90
                                                                                GCCCACCAGGAACTTCTCAAAGTTCCAGGCAACNTCGTTGCGACACACCGGAGACCAGGTGATNAGCTTGGG
230 280 280 290
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250 Mismatches
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US-08-904-809-21 Sequence 21, Application US/08904809
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Matches
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31
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#### 1260 AAAAAAAA

41. US-09-030-606-173 (1-1265) US-09-020-747-26 Sequence 26, Application US/09020747

Initial Score = 56 Optimized Score = 239 Significance = 0.33
Residue Identity = 32% Matches = 271 Mismatches = 541
Gaps = 19 Conservative Substitutions = 0

' '' ABCAGNGACCNNNAACTGCNGCCTGGGACAGCNCTGGGANCAGCTAACNNAGCACTCACCTGCCCCCC CNACCAGNGACCNNNAACTGCNGCCTGGGACAGCNCTGGGANCAGCTAACNNAGCACTCACCTGCCCCCCC 380 430 440

1250 X TAAGAGANGNGCAAAAAAAA us-09-030-606-173.res

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Page

CCCCNNNTCCTTTNCCC 810 820

(1-1265) Sequence 94, Application US/09020747 42. US-09-030-606-1 US-09-020-747-9

305 Significance Mismatches Optimized Score = 162 Matches = 186 Conservative Substitutions 55 368 21 Initial Score Residue Identity Gaps

510 AGGTCTGCAGTAAGC

(1-1265) Sequence 26, Application US/08904809 43. US-09-030-606-173 US-08-904-809-26 3

Significance Mismatches Optimized Score = 239
Matches = 271
Conservative Substitutions. 32**%** 32**%** 19 Initial Score
Residue Identity Gaps

ANATTANTACAGTGTAATCTTT X

--GAGGAGGTCTGCAGTAAGCTCTATGACC 460 470 400 CTACCGTGCTGCAGTGCGTGGTGTCT-

GCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAAC

770

TAAGAGANGNGCAAAAAAAAA

us-09-030-606-173.res

| 360 | 360 | 370 | 380 | 400 | 410 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 210 220 230 240 250 260 270 CCCAGAGTACAAGTTGGACGAATCCGTGTCCGAGTC 180 290 300 310 320 340 TGACATTG-CTTCGCAGTGCCCTACCGCGGGGGAACTCTTGCCTTTGCTTTCTGGCT ACAANACCCANGANAGGCCACT X 10 70 80 90 100 110 X 120 130 GGGCGTCCTGCTGCTACACCATCGGGCT 96 Significance 105 Mismatches 45. US-09-030-606-173 (1-1265) US-09-020-747-31 Sequence 31, Application US/09020747 Sequence 153, Application US/09020747 Conservative Substitutions Optimized Score Matches 430 440 GGGGCTGACCCAGAGCTCTGCGTCC .368 44. US-09-030-606-17: US-09-020-747-15 Initial Score = Residue Identity = Gaps = 810

| 350 | 360 | 410 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 | 420 280 340 340 310 320 340 CTGACGCGGGGGAACTCTTGCTTGCTTGCCTTGGCT TTTTTTTTTTTTGGCGA ---CTATTAGAAGCA 210 220 230 240 250 x 260 270 ACCCAGAGTACAACATGCTCGTGTCCGAGT 0.30 Optimized Score = 268 Significance = 300 Mismatches = Conservative Substitutions = TGCTACTGTTTAATTGCAGGAGGTGGGGTGTGTGTACCATGTACCAGGG-----30 40 54 36% 23 Initial Score Residue Identity Gaps

1000 1010 1020 1030 1040 1050 1060 cccrccrcagagrcaaggcccccaagccccca | 840 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 ccagccctcctccagacccagaaccccagaaccccagaaccccagaaccccaaga GAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAAATA CCNTCNAANAAGTAATTCACCCCCCCCCCCTTATTGCCTGGG-----CCCTTAANTACCCACACCGGAA 450 450 470 480 CCAGGGGACCTTCTGTTCTCCCANGGNAACTTCNTNNATCTCNAAAGAACACAACTGTTTCTTCNGCANTTC 300 310 320 330 GGGTGGGAGTGGGTGGCTGGTNCNAATGGCCTGNCACANATCCCTACGATTCTTGACACCTGGATTTCA 070 x 1080 1090 1100 1110 1120 ACCCCTCGTTCCCCAGACCCAGAGGTNNAGGTCCCAGCCCTCTTCCNTCAGACCC

46. US-09-030-606-173 (1-1265) US-08-806-596-24 Sequence 24, Application US/08806596

233 Significance = 257 Mismatches = Conservative Substitutions. Optimized Score = Matches = 54 318 13 Initial Score Residue Identity =

```
NCTTGGCNTAATCATGGTCNTANCTGNCTTCCTGTGTCAAATGTATACNAANTANA
                                                370 380 390 400 410 420 430 ACGTGAGCTCACTCACGGGGGGGCTGACCCA
                                                                                                 3ACAAGANNGTATCNTNCATTAGTAACAANTGTNNTGTCCATCCTGTCNGANCANAT
10 120 130 160
 TAGNGTCACCTAAATA
                                                                                      -TATGAATCTNATNT
```

460

GAAAACCGTCCAGGCCAGTTAACTCTGGGGACT - - - GGGAACCCATGAAATTGACCCCCAAATACATCCTGC NGGCACAATGTCGNCG GGTNNCCNTGGGGGGTGAANCTCNGNNTCANCCNGNCGAGGNNTCGNAAGGAACCGGNCCTNGGNCGAAN 720 730 730 CTCCCTCAAACCAAGGGTACAGATCCCCAGCCCCTCCTCCTCAGACCCAGGAGTCCAGACCCCCAGCCCC

TCCTCCCTCAGACCCAGGAGTCCAGCCCCTCCTCCNTCAGACCCAGGAGTCCAGACCCCCCAGGCCCTCCTC 950

AANGG

(1-1265) Sequence 98, Application US/09020747 47. US-09-030-606-173 US-09-020-747-98 S

TIGGAAŢAATCITGACŢCCTGAACTIGCTCCTGCGA

CACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCA 

850 860 CCCCAGCCCTCCTCCT

US-09-030-606-173 (1-1265) US-08-904-809-38 Sequence 38, Application US/08904809 48.

0.27 479 0 Significance Mismatches Optimized Score - 208 Matches - 245 Conservative Substitutions 52 328 31 Initial Score = Residue Identity = Gaps

GCCCCAATTCCAGCTGCCACAC

	,							. •		
	610 620 630 640 650 660 670  GGCCCCTGATCTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCCAAGTTGCG	680         690         700         710         720         730         740           TGCCAGGTCACTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCT	750 760 810 GGGGACTGGGAACCCATGAATACATCCTGCGGAAGGAATTCAGGAATATCTGTTCCCAG GGGGACTGGGAACCCATGAATTGACCCCCAAATACATCCTGCGGAAGGAA	820   830   840   850   860   870   880   800	90   900   910   920   930   940   950   960	970 980 1000 1010 1020 1030 TCCTCCNTCAGACCCCAGGACCCCCCCCCCAGGGGTTGAGGCCCCCCAAC	1040 1050 1060 1000 1090 1090 1100	1110 1120 1130 1140 1150 1160 1170 CCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCACTAGATTTTCCCTGNACACAGTGCCCCTTGTGGNAN	1180 1230 1240 GTTGACCCAACTTACCAGTTGTTTTTNGTCCCTTTCCCCTAGATCCAGAAATAAAGTTTAAGA GTTGACCCAACCTTACCAGTTGGTTTTTTTTTT	
80	660 GCCCCGTGTGC	730 ACCGTCCAGG(         ATNCCTNGAAA( 210	800 AATTCAGGAAT        AATTCNCCTAA 280	820   830   840   850   860   870   860   870   800   870   800   870   800   870   800   870   800   870   800   870	940 CTCAGACCCAG     N   CGAATTTTTT	970 980 1000 1010 1020 TCCTCCNTCAGACCCCAGCCCCTCCTCAGACCCAGGGGTTGAGGTTGAGGTTGAGGGTTTGAGGGTTGAGGGTTGAGGGTTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTGGGGGCCATNCCCCCNCTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTCGGGGGTTTTTCGGGGGTTTTTCGGGGGTTTTCGGGGTTTTTCGGGGGTTTTTCGGGGGTTTTTCGGGGGTTTTTCGGGGGTTTTTCGGGGGTTTTTCGGGGGTTTTTT	1090 CAGACCCAGAG 11 1 AAGNNTTAATT	1160 GNACACAGTGC 	90 1230 1240 TTACCAGTIGGITITICATITITNGICCCITICCCCIAGATCCAGAATAAAGI	
7.0	650 CTTTCGGAAAA 111   111 ATTTTGGA	720 GGATAGAGAAA       ATNAACTTAAA	790 CTGCGGAAGG? 	860 SCCTCCTCCT(       STNAANTATTT 340	930 SCCCTCCTCC         NCCAATTAAAC	1000 CCTCCTCCTCAGA             GCCATNCCCCNCT 480	1080 CCTCGTTCCCC        AAAAACTCCCI	1150 NGATTTTCCCT 	1220 rcccttrccc        scccttnang	
09	610   620   630   640	710 ATTCACTGAGT          TTAACCCATT	780 CCAAATACATC 	850 GGCCCCCAGCC 111 1 1 TNACCCNNGNG	920 AGACCCCCA(           ANNNCCCTAAI	990 10 cccccagcccc 	agcccccaaccc             vccccaanaa	AATGCCACCTA           TNTGGGGGCC	1210 TCATTTTNG:            TGGTTTTTGG: 670	
50	620 630 GGGTACTTGCAGG           GGGGGGTTCCAAA	700 ACCTCTGCAA 11 GTNAAGAAAA 180	AAATTGACCO	840 CAGGAGTCCA THANTINTT	910 CCAGGAGTCC 	980 GAGTCCAGACC A 11 1 GGGTTTTCC	0 1060 CAGAGGTCCAA I NCCCAAAAAAN	1130 CCAGNGGTCC       AAGGNGGGTT	1200 :AGTTGGTTTT          STTATNGNNTT 660	≪.
40	610 GATCTGCAACG 	690 GTCTACACCA 11 NAANCCAAAT	760 GGAACCCATG         TTAACCC-TT	830 CCCTCAGGCC       TTAAACCCCCT	900 CTCCCTCAGAC           NTNGGTAACTC	970 TCAGACCCAG 1   1 GAATTNACCG 450	0 1050 CCTTCAGAGTCi        LTTTTNNANGN	1120 rTCCNTCAGAC         GCCTTTGGGA	1190 CCAACCTTACC	50 GANGNGCAAAAAAAAA
30	GGCCCCTG1       AAATNNCC2 90	680 TGCCAGGT( 	750 GGGGACTG   1 AAAAATTT 230	820 CCCCTCCT GTTNGATT	890 · GCCCCTCC I NTTAANCI 370	TCCTCCN      TCCNNGG	1040 CCCTCCTC GGTTGAAT	1110 CCCCTCT   11 TCCCAGG	1180 GTTGACC         GGTAA	1250 GANGNG

CG 220 230 240 250 260 X 270 280 GTACAACAGACCCTTGCTCATCATCATTGGACGAATCCGTGTCCGAGTCTGACAC 0.27 458 0 Optimized Score = 245 Significance Matches = 290 Mismatches Conservative Substitutions sequence 12, Application US/08904809

49, US-09-030-606-173 (1-1265) US-08-904-809-12 Sequence

ccceecnceccc 720 x

52 378 18

Initial Score
Residue Identity = Gaps

```
930 940 1000

CCTCCTCCAGACCCAGGAGTCCAGCCCTCCTCCTCC

CCTCCTCCTCAGACCCCAGGAGTCCAGCCCCTCC

CTCTCCTCAGACCCCCTCCTCCTCCTCCTCCTCC

CTCTCTCAGACCCCAGGAGTCCAGACCCCTCC

CTCCTCAGACCCTCCTCCTCTCTCTCTCTCTCTNAANNAANGAAC

CCTCCTCAGACCTGCTCTCTCTCTCTCTCTNAANNAANGAAC

660 670 680 690 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1010 1020 x 1030 1040 1050 1060 1070 TCCCTCAGAGACCCCCCAACCCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                               790 800 810 820 830 840 850 GCGGGAAGGAATTCAGGAATATCTGTTCCCAGCCCTCCTCAGGCCCAGGAGTCCAGGCCCCAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650 660 670 680 690 700 710
TTCGGAAAAGCCCCGTGGCCAAGTTGCCGTGCCAGGTGTCTACACCTCTGCAAATCACTGAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                 AATGAAGATGANGAGAAGAAGGTCNCGAGGGCACACTTGCTCTCAGTÇTTANCACCATANCA
380 390 400 410 420 430
                                                                                                                                                                                                                                                                                                                         0 580 530 640 610 620 630 640 cagaactcrigcaacgciccrigaictriciacaacgciccrigicicri
                                                                                                                                                CACCCACGGTGACTGCATAGTTCGGA-TGTCATACAAAAGCTGATTGAAGCAACCTCTACTTTTTGGTCG
CACCCACGGTGACTGCATTAGTTCGGA-TGTCATACAAAAGCTGATTGAAGCAACCTCTACTTTTTTGGTCG
70 80 90
```

50. US-09-030-606-173 (1-1265) US-08-806-596-22 Sequence 22, Application US/08806596 Initial Score = 52 Optimized Score = 255 Significance = 0.27
Residue Identity = 34% Matches = 303 Mismatches = 530
Gaps = 34 Conservative Substitutions = 0

 CCGNCTTCCNACCCANGNNTTCCNCGAGGACACNNNACCCCGCCNNCANGCGG

51. US-09-030-606-173 (1-1265) US-09-020-747-38 Sequence 38, Application US/09020747 Initial Score = 51 Optimized Score = 208 Significance = 0.25
Residue Identity = 328 Matches = 245 Mismatches = 479
Gaps = 31 Conservative Substitutions = 0

TGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCT

| 990 | 910 | 920 | 930 | 940 | 950 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960 | 960

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GGATAGAĞAAAACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAAATACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 650 650 670 680 690 700 710 CITTCGGAAAAAGCCCCGTGTGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTGGAAATTCACTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 370 380 400 410 420 GGTCTGCCTGTCTAAGGAGGTCCTCTGCCCAGTCGCGG
                                                                                                                                                                                                                                                                                                                                                                            430 440 450 460 470 480 490 GGGCTGACCGTGCTGCAGGGTGAACGTGTCGGTGGTGT
                                                                                                                                                                                                                                                                     300 310 320 330 340 350 ATCAGCATTGCTTGCCTCGTTGCTTGGCTGG
                                                                                                                                                                                                                                                                                            CATTICCGGGTTTACTTICTAA.
                                                                                        1110 1120 1130 1140 1150 1160 1170 ccccrctrcorragacccagngsccargccaccagnacacagrgcccccttgtagnan
0.25
494
0
                                                                                                                                                                                                                                   Optimized Score = 253 Significance
Matches = 305 Mismatches
Conservative Substitutions
                                                                                                                                                                                                           52. US-09-030-606-173 (1-1265) .
US-08-806-596-8 Sequence 8, Application US/08806596
                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTGGGACACATCGCGAGTACGAACAGCGCCTGAA------190
                                                                                                                                                                                                                                  Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810
                                                                                                                                                                                                                                       51
358
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               730
                                                                                                                                                   950 1260
GANGNGCAAAAAAAAA
                                                                                                                                                                                                                                                                           30 290
GACACCATCCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCAGTGTAGCCG
220
                                                                                                                                                                                                                                      Initial Score Residue Identity Gaps
                                                                                                                                                                            ccceednceecce 720 x
                                                                                                                                                     1250
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GATCTGCAACGGGTACTTGCAGGGCCTTGTGTTTCGGAAAAGCCCCGTGTGGCCAAGTTGGCGTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 480 490 500 510 520 530 cgrgcrgcagrgcrgcagrgcrgcagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcrgcagraccagrgcagraccagrgcagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccagraccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCAGCATGTTCTGCGCCGGGGGGGGGAGGACCAGAAGGACTCCTGCAACGGTGACTCTGGGGGGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCCTGCCCAACCTGATCTGATGACTGCGGATGCTG-TGACGGACCCAAGGGCCAAATAGGGTCCCAGGG 100 110 120 130 140 140 150 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00 410 420 430 440 450 460 AGGAGGTCCTGCCTCCCAGGCAGAATGCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 340 350 360 370 380 390
GAACTCTTGCCTCGTTTCTGGCTGGGGTCTGCTGCTGTGTGTGTGTGTGTGTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rcressrearsscrerrcre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCNCNNCNNCNANCCGACCCNNANNTTNNANNNCCTGGGGGTNCCNNCNGATTGACCCNNCCNCCCTNTA 720 730 740 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00 1010 1020 1030 1040 1050 1060 1070 CCTCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTAATNNCGCCTTGGCCTTNCCANNGTCCTNCNTTTTCCNNTGTTNAAATTGTTANGCNCCCNNT
620 630 640 650 650 660
                                                                                                                                                                                                                                          GGAGTGTTCTCCTTACAACCACANNATGCCGGCTCCTCCGGAAACCANTCCCANCCTGNGAAGGATCAAG
520 540 500 500 510
                                                                                                                                                                           CTGCGGAAGGAATTCAGGAATATCTGTTCCCAGCCCCTCCTCCTCAGGCCCCAGGAGTCCAGGCCCCCAGGCC
                                                                     -retrigangigadececargicaretageceaergrengaecaeertring
470 480 440 450 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Significance = Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-1265)
Sequence 27, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score = 241
Matches = 270
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
32%
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1220 1230 ccttrccctagarccaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53. US-09-030-606-173
US-08-904-809-27 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Score Residue Identity Gaps
                                                                                                   Treccrre-
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CTCCNNTCTCCGGCCNC X

(1-1265) Sequence 19, Application US/09020747 54. US-09-030-606-17 US-09-020-747-19

0.23 n i n 201 Significance 235 Mismatches Conservative Substitutions Optimized Score Matches Initial Score = Residue Identity =

CNAAGCTTCCAGGTNACGGGCC x 20 00 510 GGAGGTCTGCAGTAAG

TCCTCCCTCAGACCCAGGGGTTGAGGCCCCCAACCCCTCCTTCAGAGTCAGAGTCCAAGCCCCCAACC CACTCANTTGTCACC - TGNCTGCTCAAGTAAAGTGTACCCCATNCCCAATGTNTGCTNGATGTCTGNCCT GACGT 460 470 470 520 1040 1030 1020

 55. US-09-030-606-173 (1-1265) US-08-806-596-34 Sequence 34, Application US/08806596

0.23 459 Significance Mismatches Optimized Score = 231 Matches = 257 Conservative Substitutions 50 35% 10 Initial Score = Residue Identity = Gaps = =

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570 580 590 600 610 620 630
ACCAGAAGGACTCCTGCAACGGTGACTCTGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCT---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCCACGCCNACATING 740 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial Score = Residue Identity = Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 510 520 530 540 x 550 560 CTGAGGAGGACCTGTACCACCCCAGCATGTTCTGCGCCGGGGGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGCGACCGCATGTACGAGC x 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sccttggcgttatcatggtcacnccngttncctgtgttgaaattnttaacccccaCA 710 720 x 730 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1070 1080 1090 1100 1110 1120 1130 caaccetegetectegetecaargee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 860 | 870 | 880 | 990 | 910 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCAGCTCAAATGCTACTTTGATTACAANGAGCAGCTCCCCGAGTCAGCCTATATGCACCAGCTCTTG
240 280 280
                                                                                                                               Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -173 (1-1265)
-34 Sequence 34, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 231
Matches = 257
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
35%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTCCACGCCNACATING 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score
Residue Identity *
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGTTNATTGCCC
670 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56, US-09-030-606
US-08-904-809
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500 510 520 530 540 x 550 560 crgadagagateretecagegagagaaagateaagagagaaagataagagagaaagagaaagagaaagagaaagagaaag
                                                                                                                                                                                                                                                                        1070 1080 1090 1100 1110 1120 1130 caacccrcrcrcrccagacccagacccagaggrccaargcc
                                                                                                                                                                                                                     0.23 \\
459
                                                                                                              640 650 660 670 680 690 700
GTGTCTTTCGGAAAAGCCCCGTGTCGCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACT
                                                                                                                                                                                                                                                                                                                                             Significance
Mismatches
                                                                                                                                                                                                                                                                                                                               57. US-09-030-606-173 (1-1265)
US-09-020-747-34 Sequence 34, Application US/09020747
                                                                                                                                                                                                                                                                                                                                             Optimized Score = 231
Matches = 257
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                 50
35%
10
```

AGGGTTNATTGCCGCCCTTGGCGTTATCATGGTCACNCCNGTTNCCTGTGTTGAAATTNTTAACCCCCACA 570 580 590 600 610 620 630 ACCAGAAGGACTCCTGCAACGGTGCTTGCAGGGCCTT---T 710 720 730 740 750 760 770 GAGTGGAACCCATGAAATTGACCCCAAATA 930 940 950 960 970 980 990 CCCCCAGCCCTCCTCCNTCAGACCCAGGAGTCCAGACCCCCA 1160 1170 1180 1190 1200 inacacagegececttgegenerges CAACCCCTCGTTCCCCAGACCCAGAGGTNNAGGTCCCAGCCCCTCTTCCNTCAGACCCAGNGGTCCAATGCC 1090 640 650
GTGTCTTTCGGAAAAGC
| | | | | | | |
TAGTTCTTCTGGAGCTC CCCCGGATNCNCTAGE GCCCAGCTCAAATGCT 240 1140 1150 ACCTAGATTTTCCCTG ATTCCACGCCNACATT 40 750 1080 100 1070

58. US-09-030-606-173 (1-1265)
US-08-806-596-36 Sequence 36, Application US/08806596

Initial Score = 50 Optimized Score = 253 Significance = 0.23
Residue Identity = 34% Matches = 516

| 750 | 760 | 770 | 780 | 790 | 790 | 810 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 710 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720

```
90 640 650 650 660
GIGACICIGGGGGGCCCTGATCIGCAAGGGTACTIGCAGGGCCTIGIGICTITCGGAAAAGCCCCGIGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 320 330 340 350 360 370 TTGGCAGTGTGCTGGCGAACGTGAGCTCAC
                                                                                                                                                                                                                                                                                                                            CACIGCCIATATGGTGTCTGCCGCAGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGAC 730 710 720 730
                                                                                                                                                                                                                         30 40 50 60 70 80 90
GGCAGGCGGCACTGGTCATGGAAAACGAATTGTTCTGCTCGGCGTCCTGGTGCATCCG--CAGTGGGTGCT
| || || |
                                                                                                            x 10 20
GGCAGCCGCACTCGCAGCCCT
                                                                 0.23 \\ 767
 CTCAGACCCAGAGTCCAGACCCCCCAGCCCCTCCTCCTCAGACCC
                                                                 Significance
Mismatches
                                                    US/08850713
                                                                  Optimized Score = 423
Matches = 486
Conservative Substitutions
                                               (1-1265)
Sequence 16, Application
890 x 90
TCCCCAGCCCCTCCTCC
                                                59. US-09-030-606-17:
US-08-850-713-16
                                                                      Initial Score = Residue Identity =
                   NGAAAACCACNCN
810 X
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CCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCCAAATGATAAATTCCAAATGCTGTTACCCAA
1600 1610 1620 1630 x 1640 1650 1660
                                                                                                                                                                                                                                                                                                    1090 1100 1110 1120 1130 1140 1150 CCCAGAGGTUNAGGTCCAGAGCCCAGAGGTCCAGAGCCCAGAGGTCCAGAGTTTTCCCTGNAC
                                                                                                                                                                                                                                                                                                                                                                               AGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTTGGGTAGGGTGGGGGATCCCCAAC
450 1460 1470 1480 1490 1500
                                                                                                                                                                                                                                                     ATCTGTTCCCAGCCCCTCCTCAGGCCCAGGAGCCCCCAGCCCCTCCTCAAACCAAGGG
                                                                                                                                                                                      880 890 900 910 920 940
T---ACAGATCCCCAGCCCTCCTCCTCAGACCCAGGAGTCCAGACCCCCAGCCCTCCTCAGACC
                                                                      740 750 760 770 780 790 800 CCAGTTAACTTCTGGGGAAGGAATTCAGGAAT
olo (120 ) 150 (120 ) 150 (120 ) 150 (120 ) 150 (120 ) 150 (120 ) 150 (120 ) 150 (120 ) 150 (120 ) 150 (120 )
                                                                                                         -GGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCAC
090 1100 1110 1120 1130 1140
                               TTATACAGGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATACCAGGCTCAG
TTATACAGGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATACCAGGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Significance
Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-030-606-173 (1-1265)
US-09-020-747-15 Sequence 155, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score = 105
Matches = 120
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
38%
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTAGGGTGTTGAAGGAAGGT
1670 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial
Residue
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 09
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61. US-09-030-606-173 (1-1265) US-08-904-809-20 Sequence 20, Application US/08904809 Initial Score = 49 Optimized Score = 216 Significance = 0.22
Residue Identity = 30% Matches = 234 Mismatches = 520
Gaps = 19 Conservative Substitutions = 0

| 510 | 520 | 530 | 540 | 550 | 560 | 570 | 560 | 570 | 560 | 570 | 560 | 570 | 560 | 570 | 560 | 570 | 560 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570

ACACAGTGC

62. US-09-030-606-173 (1-1265) US-09-020-747-20 Sequence 20, Application US/09020747 Initial Score = 49 Optimized Score = 216 Significance = 0.22
Residue Identity = 30% Matches = 234 Mismatches = 520
Gaps : 0

 | 510 | 520 | 530 | 540 | 550 | 560 | 570 | 160 | 160 | 160 | 170 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180

| 810 | 820 | 830 | 840 | 850 | 860 | 840 | 850 | 860 | 860 | 810 | 850 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860

| 940 | 950 | 960 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 101

CCNTTGNAGGCCCCCTNNCGGG 730 740 750 X

1160 ACACAGTGC 63. US-09-030-606-173 (1-1265) US-08-806-596-15 Sequence 15, Application US/08806596 Initial Score = 49 Optimized Score = 259 Significance = 0.22 Residue Identity = 39% Matches = 326 Mismatches = 450 Gaps = 53 Conservative Substitutions = 0

AAANCTNCCCCCCC

64. US-09-030-606-173 (1-1265) US-09-020-747-24 Sequence 24, Application US/09020747 CGGAANGG 810 x 5. US-09-030-606-173 (1-1265) US-09-020-747-35 Sequence 35, Application US/09020747 Initial Score = 49 Optimized Score = 266 Significance = 0.22 Residue Identity = 35% Matches = 293 Mismatches = 524 Gaps = 20 Conservative Substitutions = 0

| 590 | 600 | 610 | 620 | 630 | 640 | 650 | 660 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650

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AAGGCACTGCCCAAAATNNCCC
X 10 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 1020 1030 1040 1050 1060 1070 1080 ACCCAGGGGTTGAGGCCCCCCAACCCCTCGTTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGGGG 170 180 190 200 210 220 220
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                                                                                                                               GGGCCGGGTTCAAANTCCCTCCNTTGNCNNTCNCCTCGGGCCATTCTGGATTTNCCNAACTTTTTCCTTCCC 710 720 730
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Matches = 106 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 (1-1265)
12 Sequence 12, Application US/09071710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s (1-1265)
Sequence 13, Application US/08850713
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CCTAGATCCAGAAATAAAGTTTAAGAGANGNGCAAAAAAAAA
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US-09-071-710-
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ACCAAGGGTACAGA
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US-08-850-713-1
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1020 1030 1040 1050 1060 1070 1080 CAGGGGTTGAGGGTCCAAGCCCCTCGTTCCCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                      70 880 890 900 910 940
ACCAAGGGTACAGATCCCCAGCCCTCCTCCGTCAGACCCAGGAGTCCAGCCCCCAGCCCTCCTCCTCCTTC
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X
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                                                                                                               CTACCCCAACTTTCCCCAACTTTCCCCACAGCTCCACAACCTGTTGGAGCTACTGCAGAC
30 40 50 50 60 70 80 90
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                                                                                                                                                                                                                                                                                                                                     Optimized Score = 101 Significance = Matches = 106 Mismatches = Conservative Substitutions
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250 250 250 x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (1-1265)
Sequence 12, Application US/09841894A
                                                                                                                                                                                                                                                                                                           68. US-09-030-606-173 (1-1265)
US-09-525-397-12 Sequence 12, Application US/09525397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 1240 1250 1260
ATCCAGAAATAAAGTTTAAGAGANGNGCAAAAAA
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ATCCAGAAATAAAGTTTAAGAGANGNGCAAAAAA
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368
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368
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US-09-841-894A-1
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us-09-030-606-173.res

(1-1265) Sequence 31, Application US/08904809 73 70. US-09-030-606-1 US-08-904-809-3

0.20 497 0 Significance Mismatches Optimized Score - 268
Matches - 300
Conservative Substitutions Initial Score
Residue Identity Gaps

580

570

AGCCCCTCCTCCTCAAACCAAGGGTACAGATCCCCAGCCCCTCCTCCTCAGACCCAGGAGTCCAGACCCC

Sequence 15, Application US/09071710 (1-1265)71. US-09-030-606-173 US-09-071-710-15 S

0.20 770 0 Significance Mismatches Optimized Score - 429
Matches - 480
Conservative Substitutions 48 378 44 Initial Score Residue Identity Gaps GGCAGCCGCACTCGCAGCCCT TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAG

GGCAGGCGCCACTGGTCATGGAAAACGAATTGTTCTGCTCGGCGTCCTGGTGCATCCG--CAGTGGGTGCT

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820 830 840 850 860 870
AGCCCTCCTCAGGCCCAGGCCCCCAGCCCTCAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  880 890 900 910 920 940 940 AGGGT---ACAGATCCCAGCCCTCCTCCTCAGACCCAGGAGTCCAGACCCCAGCCCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                   730 740 750 760 770 780 790 800 CAGGCCAGTTAACTCTGGGGAAGGAATTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 670 680 690 700 710 720
TGTGGCCAAGTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTC
                                                                                                                                                                                                                                                                                                                                                      rcrcragggcrgccrgacrgcaggccrrccaagggggrrrcagrcrgacrraracag
970 980 990 1000 1010
                                                                                                                                                                                                                                                                       00 610 620 630 640 650
segecccrearcrecaacegeracriccaaegeccrrerererrregeaaaageccce
                                                                                                                                                                                                                                                                                          AATGTGGCTCTCTGCTGCTGCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGCTGGGGCGTCCCTC

880 890 940
                                                                                                                                                                                                                                       CACTGCCTATATGGTGTCTGCTGGTCGCCATTTACTTTGCTACACGGTAGTATTTGA 730 690 690 700 710 720 730
                                                                                                                                                                   200 210 220 230 --CCTCCCGTACGCCACAGACCCTTGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTG---
1100 1110 1120
                                                                                                                                                                410
  170 180 190
GCCAGGGAGCCAGATGGTGGAGGCCAG-
                                                                                                                                                                                                                                                                                                                                                       rccrcrcrcccAGT(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATATCTGTTCCC
                                                                                                                                                                                                                                                                                                                                   590 60
AACGGTGACTCTGGG
                                                                                                                 300
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1060

1020

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240 250 260 270 280 290 TAACGACTCATCATCCGGAGCATC----AG
                                                                                                                                                                                                                                                                                                                                                                  170 180 190 200 210 230 230 GCCAGGGAGCCAGAGGAGCCCTTGCTCGC
                                                                                                                                                                                                                                                                              TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAG
330 340 350 350 370
                                                                                                                                                                                                           X
GGCAGCCCGCACTCGCAGCCCT
                                                                                                  GACCCAGGGGTTGAGGCCCCCAACCCCTCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCC
         0.20
                                                                                                                                                                                 Significance
Mismatches
                                                                                                                                                                      Sequence 15, Application US/09525397
                                                                                                                                                                                  Optimized Score = 429 :
Matches = 480 I
Conservative Substitutions
                                                                                                                                           CCAAGGTTAGGGTGTTGAAGGAAGGT
1660 1670
                                                                                                                                                                  (1-1265)
                                                                                                                                                                                     48
378
44
                                                                                                                                                                   US-09-030-606-173
US-09-525-397-15
                                                                                                                                                                                       N 11 B
                                                                                                                                                                                     Initial Score Residue Identity = Gaps
```

us-09-030-606-173.res

SGCCTGCCTCACTGG 190 800	510 54GGTCTGCAGT              : GTTGCTGCCAAGT   870	) 580 SAGACTCCTGC SAGGGCTCCTC SCTGGGGCGTCCCTC 940	650 TCGGAAAAGCCCCG         CTGGACTTATACAG	720 NTAGAGAAACCGTC 	790 800 TCCTGCGGAAGGAATTCAG	860 TCCTCCCTCAAACCA 	930 940 AGCCCTCCCTCA         AGTCCTGAGGGCAAC 1280 1290	00 CCTCCCTCA 	1070 1080 CAACCCTCGTTCCC	140 1150. ACCTAGATTTTCCCT         AGGGTGGGGGATCCC	1210 TTCATTTTINGTCCC 	
CAAGAGCGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT	450         460         470         480         490         500         510           GTCCCAGGCAGAATGCCTACCGTGCTGCTGCTGAGGAGGTCTGCAGT         1         1   1   1   1   1   1   1   1   1   1	520   530   540   550   560   570   580	590         610         620         630         640         650           AACGGTGACTCTGGGGGCCCTGGTGTTTTCGGAAAAGCCCCG         1	660         690         700         710         720           TGTGGCCAAGTTCTACACCTCTACACTCTCTACTCACTGATAGAGAAAACCGTC           I	0 CCCCCAAATACA	810   820   840   850   870	880 890 900 910 920 930 940  AGGGTACAGATCCCCAGCCCTCCTCCTCCTCAGAGCCCCCCCCCAGCCCCTCCTCCTCCTCCTCCTCCTCCTCCTCAGAGCTCCAGACCCCCCCC	950 960 970 980 990 1000 GACCCAGGAGTCCAGACCCCCCCCCCCCCCTCCTCCCTCA	1020	CAGACCCAGAGGTNNAGGTCCCAGCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCACTAGATTTTCCCT         1150.           CAGACCCAGAGGTNNAGGTCCCAGCCCAGNGGTCCAATGCCACTAGATTTTCCCT	1160	TTTCCCTAGATCCAGAAATAAAGTTTAAGAGANGNGCAAAAAAAAAA
TGGCCAAATACTCAGCGTAGAA 750 760	460 470 AATGCCTACCGTGCTGCAGTGC	530 540 CCCGCTGTACCACCCAGCATG	600 610 TGGGGGGCCCTGATCTGCAAC	670 680 690 TGGCGTGCCAGGTGTCTACACCA. 	30 740 750 760 770  CAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAATTGA	820 830 cccacccrccrcaegc                      cccarcrcraagcccrraacc 0 1170 1180	890 900 SATCCCCAGCCCTCCTCCTC 	960 970 CCAGCCCTCCTCCNTCAGACC                   AGGTCCCTCAGCCCACAGCAC	0 1030 1040 TGAGGCCCCCAACCCCTCCTCC 	1110 GTNNAGGTCCCAGCCCTCTTC 	1170 CCCCTTGTGGNANGT              TCCCCTGAGATAGCTGGTCATT 0 1530 1540	1230
CAAGAGGGACT 740	450 GTCCCAGGCAG         GTCCCAGCTCC	520 AAGCTCTATGA 	S90 AACGGIGACTC	660 TGTGGCCAAGT'   1 1 1 GGAGGCCAGAA	730 740 CAGGCCAGTTAN           CTAGCCTCCTAG	810 GAATATCTGTT 	880 AGGGTACA( 111   111 AGGATGAAACA( 1230	950 GACCCAGGAGT        ACACAAGAACC	010 GACCCAGGGGT'           GGATGTGGCCT' 1370	1090 CAGACCCAGAG           ACAAAGTAGAA	1160 1170 GNACACAGTGCCCCTTG	1220 12 TTTCCCCTAGA

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00 310 320 330 340 350 350 370 CATTGCTTCGCAGTGCCTGGCGAACGGTGA
                                                                                                                                                                                                                                                                                                                                                                                           590 600 610 620 630 640 650 AACGGTGACTCTGGGGGCCCTTGTTGGGAAAAGCCCCG
                                                                                                             x 10 20 GGCAGCCGCACTCGCAGCCCT
                                                                                                                                     . TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAG
300 310 320 320 330 370
                                                                                                                                                                                                                                  rcerciceccagiereragggergecraacigaggeerircaaggggrireagrergaerraracag
950 950 1000 1010
                                                                           0.20
                                                                           Optimized Score = 429 Significance = Matches = 480 Mismatches = Conservative Substitutions =
1640
                                                 73. US-09-030-606-173 (1-1265)
US-09-841-894A-1 Sequence 15, Application US/09841894A
1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470
                CCAAGGTTAGGGTGTTGAAGGAAGGT 1660 1670
                                                                            48
378
44
                                                                             8 B B
                                                                           Initial Score
Residue Identity
Gaps
```

GCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 1630 1640 1650 1650 1090 1100 1120 1130 ,1140 1150.
CAGACCCAGAGGTNNAGGTCCCAGCCCTCTTCCNTCAGACCCAGNGGTCCAATGCCACTAGATTTTCCCT ACACAAGAACCAGGTCCCTCAGCCACAGCACTGTTTTTGCTGATCCACCCCCTCTTACCATTTATCA 1300 1310 1320 1330 1340 1350 1350 CCCCTCCTCCNTCAGACCCAGGAGTCCAGACCCCCCAGCCCCTCCTCCC----TCA | 810 | 820 | 840 | 850 | 860 | 870 | 860 | 870 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 880 890 900 910 920 930 940 AGGGT----ACAGATCCCAGGCCCTCCTCCTCCTCA IGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTC GACACACCTAGAGAAGGGTTTTTG---1110 1120 1130 TGTGGCCAAGTTGGCG CAGGCCAGTTAACTCT | || || || || CTAGCCTCCTAGTTGA GACCCAGGAGTCCAG 1010

GGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAG 350 350 370 30 60 70 80 90 90 GGCAGGCGGCGTCCTGGTGCATCGT-CAGTGGGTGCT x 10 20 GCCGCCGCACTCGCAGCCCT 0.20 Significance Mismatches US/09071710 Optimized Score = 429
Matches = 487
Conservative Substitutions 74. US-09-030-606-173 (1-1265) US-09-071-710-16 Sequence 16, Application Initial Score = Residue Identity = Gaps TCCCTCTACCACC

GGCCAAGTTGGCGTGCCAGGTGTCTACACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAG

CCAAGGTTAGGGTGTTGAAGGAAGGT 1660 1670

TAACGACCTCATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACCATCCGGAGCATC----AG

us-09-030-606-173.res

AGGTTAGGGTGTTGAAGGAAGGT 1670

(1-1265) Sequence 16, Application US/09525397 75. US-09-030-606-173 US-09-525-397-16 S

X 10 20 GGCAGCCGCACTCGCAGCCCT 0.20 0 Optimized Score = 429 Significance Matches = 487 Mismatches Conservative Substitutions 48 378 37 Initial Score
Residue Identity

CATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATC----AG TAACGACCTCATGCT 240

1010 970

CCAGGGGTTGAGGCCCCCAACCCCTCCTTCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCAG 1040

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| 590 | 600 | 610 | 620 | 630 | 640 | 650 | 640 | 650 | 640 | 650 | 640 | 650 | 640 | 640 | 650 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 
TAATGTGGCTCTCTGCTGCCACCCTG-
890 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1160 1170 cacagreeccccrrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ji li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 460 470 480 490 500 510 GICCCAGAATGCCTACCGTGCTGCAGAACGTGTCGGTGTCTGAGGAGGTCTGCAGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 530 540 550 560 570 580 CICTATGACCCGCTGCAGGCAAGACCAGAAGGACTCCTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 390 400 410 420 430 440 GCTCACGGGGGGGGGGCTGACCCAGAGCTCTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X 10 20 .. GGCAGCCGCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAG
310 320 330 340 350 350
                                                                            0.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09841894A
                                                --TGGNANGTTGACCCAACCTTACCAGTTGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Optimized Score = 429
Matches = 487
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score
Matches
                         1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-1265)
                                                                                                                                                                                                                                                                                                                                                                         AGGTTAGGGTGTTGAAGGAAGGT
1670 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76. US-09-030-606-173
US-09-841-894A-1 $
                    1160 1170
CACAGIGCCCCCTIG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score Residue Identity Gaps
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1020 1030 1040 1050 1060 1070 1080 CCAGGGGTTGAGGCTCCTCTTCAGAGTCAGGGTCCAAGCCCCTGTTCCCCAGGTTCTTCCCAGGGTTTGAAGCTTTGAAGCTTTAAATATTTAATTTAACA 1380 1440 1410 1420 1430 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCA 1600 1610 1620 1630 1640 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1090 1100 1110 1120 1130 1140 1150 ACCCAGAGGINNAGGICCCAGCCCTCTTCCNTCAGACCCAGAGGICCAATGCCACTAGATTTTCCCTGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TGGNANGTTGACCCAACCTTACCAGTTGGTTTTTCATTTTTNGTCCCTTT
                                                                                                                                                                                                                                                                                                               CAAGAACCAGGTCCCTCAGCCACAGCACTGTCTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGA 1310 1320 1330 1340 1350
                                                                                                                                                                       CCAGGAGTCCAGCCCTCCTCCNTCAGACCCAGGAGTCCAGACCCCCCAGCCCCTCCTCCC----TCAGAC
                                                                      0 670 680 690 700 710 720 730 GGCCAAGTTGGCTGGGATAGAAAAACCGTCCAG
                         Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77. US-09-030-606-173 (1-1265)
US-08-850-713-6 Sequence 6, Application US/08850713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGTTAGGGTGTTGAAGGAAGGT
1670 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score
Residue Identity
```

S

78. US-09-030-606-173 (1-1265) US-09-071-710-4 Sequence 4, Application US/09071710 Initial Score = 47 Optimized Score = 81 Significance = 0.19
Residue Identity = 42% Matches = 85 Mismatches = 116
Gaps = 1 Conservative Substitutions = 0

 250 CATGCTCATC 79. US-09-030-606-173 (1-1265) US-09-525-397-4 Sequence 4, Application US/09525397

Initial Score = 47 Optimized Score = 81 Significance = (
Residue Identity = 42% Matches = 85 Mismatches = 1 Conservative Substitutions = = 1

X 10 20 GGCAGCCGCACTCGCAGCCCTGGCA

250 CATGCTCATC 80. US-09-030-606-173 (1-1265) US-08-850-713-5 Sequence 5, Application US/08850713 Initial Score = 47 Optimized Score = 81 Significance = 0.19
Residue Identity = 42% Matches = 85 Mismatches = 116
Gaps = 1 Conservative Substitutions = 0

GGGCTCCATTGTCCAGCTCAGCCAGTCTGTCA

250 CATGCTCATC

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> 0 < O | O IntelliGenetics > 0 <
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Results file us-09-030-606-173-inv.res made by tport on Thu 1 May 103 14:59:42-PDT.

g compared:US-09-030-606-173' (1-1265)
searched:
ve cutoff: Query sequence being Number of sequences Number of scores abo

initial comparison of US-09-030-606-173' (1-1265) with: 79-67 Results of the File: 613004 File: 625204 File: US0880 File: US0895 File: US0902 File: US0902 File: US0908 SCORE 0 STDEV 100-NUMMACN OE SECRECES

## PARAMETERS

K-tuple Joining penalty	Window size	
Unitary $1$	5.00 0.33 1	
Similarity matrix Mismatch penalty	<pre>Gap penalty Gap size penalty Cutoff score Randomization group</pre>	

30 500

## SEARCH STATISTICS

-			
1	Standard Deviation 14.46	Total Elapsed 00:00:01.00	-
	Median 30	•	189792 410 410
	Mean 29	CPU 00:00:01.89	Number of residues: Number of sequences searched: Number of scores above cutoff:
	Scores:	Times:	Number of Number of Number of

The scores below are sorted by initial score. Significance is calculated based on initial score

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

тате	! ! !	0 (	00	0	0	0	c	•	0	0	00	0	0	c	0	0	00	00	0	0	<b>&gt;</b> c	0	0	0	<b>&gt;</b> C	0	0	0 0	0	0	00	0	0	<b>&gt;</b> C	0	0	00	0	0	<b>-</b>	0	0	<b>-</b>	0	0 0	0	0 0	00
Sig. F		ο.	4.49	0	٥.	3.80	r	2.35	ω.	w.	. c	, 0	٥.	100	1.94	ω.	œ, ο	9 00	. &		· •	9	ı.	ເບັ ເ	ບົດ	jυ	υ,		. 4	٣.	ب. س	. w	რ.	u	. r.	Ε.	L	. w	w. c	30	. 2	٦.		-	۲.	1.11	۲	1.04
Opt. Score		8	430	8	g Q	264	u	174	m	9	on o	200	m	316	256	84	114	206	237	224	1275	290	230	405	200	257	257	281	226	16	76	8 6	89	50 O	157	1.44	. 44 275	275	239	211	253	134	134 246	233	149	242	242	72
it. ore	*	10	2, Q 4, Q	88	87	84	* 0	63	63	63	62	28	58	* * *	57	26	N N	יור	55	54	υ r 4 ω	, m	25	25	տ Վ <del>Ի</del>	51	51	5.	000	49	4 Z	4 8	48	4 	 	. 40	00 or	) oʻ	<b>.</b>	4 / 4 /	47	40	4 4 0 9	46		4 2	45	
I Length S	bove mea	1265	σ-	16	90	774	ve mea	‡ rV	~	_	אַ כ	7	820	ູ	17	CI	m <		· ω	_	יי ש	ים נ	7	14	- [	. [	_ ;	11	7		<u> </u>	1 (7)	CA (	M C	4	ľ	n α	တ	ω,	4.6	852	377	377 802	872	473	818 816	816	195
	deviations a	lication	licatio	icati	Lica	pplication	deviations a	ppication Application	pplication	pplication	Application	Application pplication	6, Application	deviation ab ppliation	Application	lication US	Application	ppiication nolication	pplication	pplication	pplication Application	Application	pplication	Application	pplication . nnlication	pplication	pplication	Application	Appitcación polication	lication US	picación o polication	pplication	pplication	pplication	pplication	pplication	pplication	at.	pplication pplication	ati	pplication	cation	ication U					
	tandard	e 173,	ce 1/1,	e 175,	e 120, andard	9 4	ğ	Ÿ	4	4	7	i i ii ii	6	ano.	1 (1)	ώ	~ C	ט ע	1	m i	Д-	- ۱	Н	-	A) (4	, <del>–</del>	, j	9,5	1 4	é	و ر	, m	'n.	<b>4</b> (	0 00	7		Ä	Cid	Ö -	44,	65,	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	23,	e 106,	e 2, Appl. e 2, Appl.	2, Ag	
ription	** 4 st	edneu	Sequenc	ednen	equen	Sequen	``;	Sequence	. ģ.	eg.	9	Sequence	Sequ	2	າ ທ.	Sequence	Sequence		, 0,	٠,٠	0, 0	, o.	. 03	9, 1		1 01	Sed	ທ ທ	Sec	O)	Sequence	LJ 1	Š	edneuc	Sequenc	Sequenc	Sequenc	Sequence	Sednence	Sequenc	Sequence	Sednenc		ednen	Sequen	dneuc	uenc	Sequence
esc	! ! !	-747-1	47-	-747-1	-747-1		* C * C * C *	0-747-34 0-747-10	-808-	-747-4	-747-	-747-3	-596-2	* FOR-1	747-1	713-6		0-608	-266-	809-3	.596-1	747-1	809-1	747-1	.5965.3 .806-3		747-1	747-1		710-6		710-3		713-4	747-8	809-7	747-7	747-1	747-2	74/-8	809-4	9-608		809-2	747-1	4-809-2	747-2	
ce Name	) ) ! ! !	-09-02	S-09-02 S-09-02	-09-02	S-09-02	06-80-sn	0 - 00 - 0	us-03-050 us-09-020	S-08-90	S-09-02	S-09-02	S-03-02 S-09-02	S-08-80	- 00 - 5	-60-	S-08-	-60	S-08-	S-08-	S-08-	-80-	5-03 S-09-	-80-	S-09-	90-	S-08-	-60-s	-60-s	S-08-	-60-	S-09-	-60-	-60-s	S-08-	-60-s	S-08-	S-09-	-60-	S-09-	S-09-8	S-08-	S-08-	200-	s-08-	S-09-		-60-s	-60-
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FastDB - Fast Pairwise Comparison of Sequences Release 5.4

580 590 GTGTAGACACCTG         1 CCAGACCCCCAG 990 .	TGCAGAT       GTCCAAG 1060 73 TGCTGGC	CAGNGGTCCAATG 1130 800 TGCAGCACGGTAG	GTTGGTTTTTCA: 1200 870 TTGAAGAGGGCA	2. US-09-030-606 US-09-020-747 Initial Score Residue Identity	Gaps	TGTCCGAGTCTG 310 32 30 30 AACTTTATTTCT	TTTCTGGCTGGG 380 390 100 ACAAGGGGCAC	CTGAGGAGGTCT 460 170 ACCTNNAC	ACCAGAAGGAC' 530 240 TGGGGGCCTCA	CTTTCGGAAAA 600 310 310 GGCTGGACTCC	GGATAGAGAAA 670 670 370
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000,000		é F	9g 23	GT	PG — 99	100 100 100 100 100 100 100 100 100 100	AGG	- GGT - GGT CATC 0	225    - 	TCA  -   CCA	TTG SAGT 980
1.04 1.04 1.04 1.04 0.90 0.90	0.83 0.83 0.76	4.98 533 0 20	GTCGC 420 90 ACNTN	GTGGT 90	AGGGCA AGGGCA 0	SGAGG	SGAGGI CACTGI	AATAC 780	CTCCT CTCCT L I I CCCCCA 850	500 STCAATTTCA          - -TCAGACCCA	AGAGG
152 190 190 253 227	113 253 122	ance = es = 10	GGTCTGCTGCCGAACGGTGAGCTCACGGGTGTGTCTGCCCTCTTCAAGGAGGTCCTTGCCCAGTCGCGG 360 370 380 390 400 x 410 420 30 40 80 50 60 70 80 90 ACTITATITITITITITICCCAGTCGTCGCGG		ACAAGGGGGCATTGTTNCAGGGAAAATCTAGGTGGCATTGGACCNCIGGGTCTGANGGAAGAGGGGGTGTGGACCACCTGGGTCTGANGGAAGAGGGGGTGTGGGGCTTGGGGCGAGGGGGAAGGGGGAAGGTGTGTTGTGCGCCGGGGGGGG	170 180 200 200 200 420 420 420 420 420 420 42	240 280 260 300 300 240 280 290 300 300 190 240 300 300 300 300 300 300 300 300 300 3	340 GGAGGGGCTCTGGACTCCTGGGT 	370 380 430 430 4430 440 420 410 420 430 CTGAGGGAGGGAGGGGCTGGGGCCTGGACTCCTGGG 430 430 CTGAGGAGGGGAGGGGCTGGGGGCCTGGACTCCTGGG 430 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	440 450 500  CCTGAGGGAGGGGCTGGGAACAGATTCCTTCCGCAGGATGTATTGGGGGCTCAATTTCA  CCTCAAGGAAGGGGCTGGAACAGATTCCTTCCCCAGGATGTATTGGGGGCTCAATTTCA	510 520 530 540 550 570 570  TGGGTTCCCAGTCCCCAGAGTTAACTGGCCTGGACGTTTTCTCTATCCACTCAGTGAATTTGCAGAGGTTG  TGGGTTCCCAGTCCCCAGAGTTAACTGCAGGAGGTTTTCTCTATCCACTCAGAGGTTG
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	7 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Significan Mismatches	GGTCCT 41 80 TAAGGT	CGTGAA 480 150	CTGANG    -  CTGCGC 550	rgactct       sgractt	290 FCCTGGC 	AAATTG	4 CTGGGG          CAGGAG 840	490 TGTATT	560 CTCAGTG
469 799 799 mean 799 818	on 196 on 327 US 799 n 400		TT CAAGGA 400 X 70 AACTGG	GCAGTG 0	Creser 	ACCTCT	TEGGAC! ACACCA 690	crccrg     11 cccarg 760	410 GAGGGG 111 CAGGCC 30	480 CGCAGGA   	ATCCAC
lon on from us on on	ton ion on		CTCTT	GTGCT 47 140	SGACCN   CCCCAG 540	GCTTGG           SATCTG 610	280 GGGGT(       TGTCT	350 CTGGA(   1	AGGGAG	4 CCTTCC 111  11	55C TTCTCT    
64, Application 1, Application 1, Application ard deviation f Application of 7, Application 7, Application	51, Application 46, Application Application US 0, Application	Score =	STCTGCC 390 60 AAATGAA	1 30 30	GGCATT    -   GTACCA( 0	TTGGGG	0 IGGCTGG 	310 320 330 340 350 GGCTGGACTCTGAGGAGGGGGCTGGGGGTCTGGACTCCTG 	400 3GTTTGA 1 3CCCTCC 820	460 470 480 AGATATTCCTGAATTCCTTCCGC	40 ACGGTT  1  ACCCAG
164, Appl 31, Appli 31, Appli dard devi 3, Applica 27, Appli	1, Ap 6, Ap Appli ', App	APPLI	rgtgt(	AGAAT	TAGGT 	AGGGG 	27 IGGAGG         IGGCGT	.340 366CTC       ACTCTC	CCCTT(	ATTCC   CCCCA 8	5 CCTGG       CTCAG
60 B 0 3 3 1 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ce 1 ce 1 ce 8, ice 9		ACGGG' 380 50 AAGGG	111 CAGGC 450	AAAATC 	190 sgaacg     sactcī	50 3AGGGA     CAAGTJ	AGGAG(       AGTTA	39 CTGTA       CTGTT	460 ACAGAT         ACAGAT 880	330 NACTGG      CCTCC
Sequence Sequence Sequence ** 0 sta Sequence Sequence Sequence	15 Sequence 14 Sequence 8 Sequence 90 Sequence 31 (1-1265)	duence 101 Ol 35% MA 42 CA	AGCTÖ	CGTCC	AGCTCT 52	rcrgg( 	26 GGTCTC   GTGGC 660	330 GAGGG   	GGGGAT	GGGAA        AGGGTA	SAGTIN               
116 31 31 31 27 27	114 114 115		ACGGTG 370 40 SATCTA	 	GTGTN(    CAGTA/ 10	180 CTGGG'     CTGCA	50 CCCTG 	) 666TCT 111 73	38 3GGCTG ITCAGG	450 GGGGCT AACCA/ 870	520 CCCCA( 
20-747- 04-809- 20-747- 06-596- 06-596- 04-809-	9-020-747- 9-020-747- 3-904-809- 9-020-747- 30-606-17-	/4 / Lty	GGCGA1 0 TTCTGC		GCACT	NACCT   1   SGACTC 580	2 CTCAAC       NAAAGC 650	310 320 330 GGCTGGACTCCTGGGGTCTGAGGGA 	70 AGGAG(       AGGAA'	440 450 ccrgaggagggggcrgggaac 	CCAGT    AGACC  920
US-09-0 US-08-9 US-08-8 US-08-8	-060-60- 0-60-sn 0-60-sn 0-60-sn	scor Scor Iden	CTGCT( 36, 30	  CTGAC  430  100	AAGGGG              	170 2Th 1 2AGAAG	240 3GGGCC   . rrcGG	O CTGGA( I II ATAGA(	3 GAGGG       GCGGA 790	440 CTGAGG 11 CTCCTC 860	510 36GTTC 
0.00	30 · 30 · 30 · 30 · 30 · 30 · 30 · 30 ·	-0 al ue	GGT	999	AC! CTC	AC( 11 AC( 57(	TG( CT'	31 66 1   6	CT	8=8	10 GG

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GACACCATCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGGGAACTCTTGCCTCG
20 330 340 350
                                                                                                                                                                                                                                                                                                   TGGATCTAGGGGAAAAGGACNAAAATGAAAAACCAACTGGTAAGGTTGGGTCAACNTNCC
                                                                                                                                                                                                                                             X 10 20
TTTTTTTTGCNCNTCTCTTA
                                                                                                                        GCCCTCCTCCTCAGACCCAGGGTTGAGGCCCCCAACCCCTCCTTCAGAGTCAGA

1000 1010 1020 1030 1640 1650
                                                                                10 600 610 620 630 640 GGCCACACACGGGCCTTTTCCGAAAGACACAAGGCCCTGCAAGTACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430
                                                                                                                                                                                                                 Optimized Score = 292 Significance
Matches = 326 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420
                                                                                                                                                                                                6-173' (1-1265)
7-17 Sequence 171, Application US/09020747
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                                                                                                                                                                   880 890 900 910
AGACACCACCGTGAGCTCACCGTTCGCCAGCAGACC
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358
44
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500 GGGTCAATTTCA      TCAGACCCA 860	570
490 GATGTATTTGC	260
480 TCCTTCGCAC            TCCTCCC	550
470 NTCCTGAAT	540
460 GGAACAGATZ 11 111111 GGTACAGATG	530
450 GGAGGGGCTG     I TCAAACCAAG	520
440 CCTGAGGGA   1  CCTCCTCCC	510
	450 460 470 480 490  \text{GGGGCTGGGAACAGATTTCCTTCCGCAGGATGTATTTGGC}

 | 800 | 810 | 820 | 830 | 840 | 850 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860

940

## 3. US-09-030-606-173' (1-1265) US-09-020-747-11 Sequence 110, Application US/09020747

Initial Score = 90 Optimized.Score = 430 Significance = 4.22
Residue Identity = 38% Matches = 490 Mismatches = 756
Gaps = 43 Conservative Substitutions = 0

| 370 | 380 | 390 | 400 | 410 | 420 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430 | 430

 | 800 | 810 | 820 | 830 | 840 | 850 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860

us-09-030-606-173-inv.res

1160   1170   1180   1190   1200   1210   1210   1220	1160	CCATGACCAGGCCTGCCAGGGCTGCCCCCCCCCCCCCCC
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1000 1010 1020 1030 1040 1050 1060
ACGGATTCGTCCAACTTGAGGAGGAGCAAGGGTCTGTTGTAGTCTGGGTGCGTACG
                                                                                                                                   CCAAATACATCCTGCGGAANGAATTCAGGAATATCTGTTCCCAGCCCCTCCTCCTCAGGCCCAGGA---G
680 710 720 730
                                                                                                                                                                                                                                                                                                                                           AGTCAGAGGTCCAAGCCCCTCGTTCCCCA-GACCCAGAGGTNCAGGTCCCAGCCCTCCTCCCT 960 970 980 1000 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAGGCTGGCCTCCACCATCTGGCTCCTGGCTCTTGGTCGGCCTCAAGACTGTGCAGGCCCAGCCCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACCAGTTGGTTTTTTTTTTTTTCCCTTTCCCCTAGATCCAGAATAAAGTNTAAGAGAAGCGCAAAAA 1100 1110 1120 1130
                                                                                                                                                                                                        650 660 670 680 700 710 GRACCCGTTGCAGGGGCCCCCCGGAGTCACCGTTGC - AGGAGTCCTTCTGGTCTTGCCCTCCGCCGG
                                                                                                                                                                                                                               ATTCACTGAGTGGATAGAGAAACCGTCCAGNCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCC 640 650 650 650 650
                                                                                                                                                                                                                                                                                                                                                                                                             500 510 520 530 540 550 560 570 AATTICATGGGTTCCAGAGTTAACTGGCCTGGACGGTTTTCTCTATCCACTCAGTGAATTTGCA
                                                                                             X 1220 1230 1240 1250 1260 AATTCGTTTTCCATGACCAGGCCTGCCAGGGCTGCGAGTGCGGGCTGC
                                                430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1170
                                                                      500
                                               400
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us-09-030-606-173-inv.res

5. US-09-030-606-173' (1-1265) US-09-020-747-12 Sequence 120, Application US/09020747	Initial Score = 87 Optimized Score = 89 Significance = 4.01 Residue Identity = 97% Matches = 88 Mismatches = 2 Gaps = 0 Conservative Substitutions = 0 600 610 620 630 640 x 650 660 GCCAACTTGGCCACAGGGCTTTTCCGAAAGACACAAGGCCCTGCAAGTACCCGTTGCAAATCAGGGGCCC	670         680         690         700         710         720         730         X           CCCAGAGTCACCGTTGCAGGAGTCTTGCCCTCCGCGGGCGCAGAACATGCTGGGGTGGTACAG         111111111111111111111111111111111111	6. US-09-030-606-173' (1-1265) US-08-904-809-47 Sequence 47, Application US/08904809  Initial Score = 84 Optimized Score = 264 Significance = 3.80  Residue Identity = 38% Matches = 310 Mismatches = 457  Gaps = 36 Conservative Substitutions = 0	340 350 360 370 380 400 GCTGGGGGGTCTGGACTCTGGGTCTGGGGAGGGGGGGGGG	410         420         430         440         450         460         470         480           GGGCTGGGGCCTGGGCCTGGGGACAGATATTCCTGAATTCCTTCC	490 500 510 520 530 540 550  GGATGTATTTGGGGGTCAATTTCATGGTTCCCAGAGTTAACTGGCCTGGACGGTTTTCTCT	560         570         580         590         600         610         620           ATCCACTCAG-TGAATTTGCAGGGTTGGTGTGGTGTGGCCAACTTGGCCACGGGGCTTTTTCC	630 640 650 660 670 680 690  GAAAGACACAAGGCCCTGCAAGTACCCGTTGCAGATCAGGGCCCCCCAGAGTCACCGTTGCAGGAGTCCTT	CTGGTCTTGCCCTCGGCGCGCGCGCGCGGGTGGTACAGCGGGTCAT-AGAGCTTACTGCAGACCT	770 780 790 800 810 820 830  CCTCAGACACCACGATCACGCACTGCAGCATTCTGCTGGGACGCAGAGCTCTGGGT	840 850 860 870 880 890 900

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CCCTTTGAGGGGTTAGGGTCCA
X 10 20
                                                                                                                                                                                           0 470 480 490 500 510 520 530 530 ABTICCTGGAGATGTATTGGGGGGTCAATTTCATGGGTTCCCAGTCCCCAGAGTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990 1000 1010 1020 1030 1040 1050 GGTGTCAGACTCGGACACGGATTCGTCCAACTTGATGAGCATGAGGTCGTTAGCGAGCAAGGGTCTGTTGTA
                                                                                                                                                  1130 1140 1150 1160 1170 1180 x 1190 TGCAGGCCCAAGCCCCATGCTAGGAGTTCTGGAAACAGTGTGCGGCTGACAGCACCCACTGCGGATGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 550 560 570 580 590 600 GGCCTGGACGGTTTTCTCTATCACTCAATTTGCAGAGGTTGGTAGACACCTGGCACGCCAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 620 630 640 650 660 670 GCACACGGGGGCTTTTCCGAAAGACACAGGCCCTGCAAGTACCCGTTGCAGATCAGGGGCCCCCCAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 Significance - 204 Mismatches -
                                                                                                                                                                                                                                                                                          GTNATCTTCACTTCTATGGCCNTCATTTGTTCTACTGCAAAATGGGGATAATAATAGT 720 730 740 X
                                                                                                                                                                                                                                                                                                                                                                                 US-09-030-606-173' (1-1265)
US-09-020-747-94 Sequence 94, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score = 167
Matches = 204
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                      1200 1210 1220 1230 AGGACGCCGAGCAGTATCGTTTTCCATGACCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                   69
38%
34
                                                                                                                                                                                                                                                                                                                                                                                                                Initial Score Residue Identity Gaps
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8, US-09-030-606-173' (1-1265) US-09-020-747-10 Sequence 104, Application US/09020747 Initial Score = 63 Optimized Score = 174 Significance = 2.35
Residue Identity = 33% Matches = 196 Mismatches = 369
Gaps = 17 Conservative Substitutions = 0

CGTAGGGGCACACCGTCAGGGCCCACCAGGAACTTCTCAAAGTTCCAGGCAACNTCGTTGCGACACACCGGA 210 220 - 270

710

680

640

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150 160 200 210
TGGGTCTGANGGAAGAGGGGCTGGGACCTNNACCTCTGGGTTGGGGAACGAGGGTTGGGGGCTTGGACCT
                                                                                                                                                                                                                                                                                                                             GIGGIATITICIGIAAGAICAGGIGIICCICCTCGIAGGIIIAGAGGAAACACCCTCAIAGAIGAAAACCC
X 10 50 40 50 70
                                                                                                                                                                                                                                                                                                                                                                                            70 80 90 100 110 120 130 140 ACTEGTAAGGTTGGTCAACATTGGACCACTGTGTNCAGGGAAAATCTAGGTGGCATTGGACCNC
                                                                                                                                                                                                                                                                                                                                                                                                                                         X 10 20 30 40 50 60
TTTTTTTGCNCNTCTCTTAAACTTTATTTCTGGATCTAGGGGAAAGGGACNAAAAATGAAAAACA
                                                                                                                                                                                                                                2.35
469
0
                                                                                                                                                                                                                                   9 1
                                                                                                                                                                                                                             Optimized Score = 233 Significance
Matches = 274 Mismatches
Conservative Substitutions
                                                                     570 X 580 590 600 610 620 ATTIGCAGAGGTIGGIGIAGACACCIGGCACGCCACACGIGGCCACACGGGGCTITICCGA
                                                                                                                                                                                    US-09-030-606-173' (1-1265)
US-08-904-809-40 Sequence 40, Application US/08904809
                                                                                                                                                                                                                                 Optimized Score
Matches
                                                                                                                                                                                                                                     63
35%
19
                                                                                                                                                                                                                                 Initial Score = Residue Identity = Gaps = =
                                                                                                                       AACACAATGG
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790 800 CGTTCACGCACTGCAGCACGGTA 10. US-09-030-606-173' (1-1265) US-09-020-747-47 Sequence 47, Application US/09020747 Initial Score = 63 Optimized Score = 264 Significance = 2.35
Residue Identity = 38% Matches = 310 Mismatches = 457
Gaps = 36 Conservative Substitutions = 0

  11. US-09-030-606-173' (1-1265) US-09-020-747-16 Sequence 168, Application US/09020747 Initial Score = 62 Optimized Score = 94 Significance = 2.28
Residue Identity = 35% Matches = 98 Mismatches = 175
Gaps = 1 Conservative Substitutions = 0

 770 780 GACACCACCGACAC 12. US-09-030-606-173' (1-1265) US-09-020-747-10 Sequence 107, Application US/09020747 Initial Score = 61 Optimized Score = 398 Significance = 2.21
Residue Identity = 35% Matches = 457 Mismatches = 801
Gaps = 39 Conservative Substitutions = 0

20 CNTCTTTA 1 AAATCCAAG	90 CAACNTNCC 	140 TGGACCNCTGGGTCT                TATGCCCGCTGAATCT 440 450	220 CTCTGACTC         ACCGCACAC 520	290 3GACTCCTGG           TTCTGTGGA 590	360 ccrgggrcrg 	430 sacrccress     sacrecrea 730	500 GTCAATTTCA GTCAATGAAGA GAAATGAAGA	570 GCAGAGGTTG             ACAGATGCCT   880	640 CCTGCAAGTA 	710 :ccrccccc      :ccrrcrrr	780   ACCGACACGT   1   1   1   1   1   1   1   1   1   1	
X TTTTTTTTTGCNCNTCTCTTA 	80 GGTAAGGTTGGG;            GGTTAGCTGGCC; 360 33	TOTAL TEGRACION OF THE CONTROL OF TH	200 TTGGGGGCTTGGA(               AATGGCTCTTTTT	280 3GCTGGGGGGTCT 	350 3GGGTCTGGACT 	420 GGCTGGGGGCCTC       ACCCCAGTTCTAC	490 GATGTATTTGGG(           GGATGATTGGCC/ 790 8(	560 ACTCAGTGAATT'               AATCTTTGACGG	630 iaaagacacaagg            caaggaacggg	700 CCTTCTGGTCTTG 	770 CCCCCAGACAC I   ATTTGGATTCAGC 1080	840
TGGGCCCAGAGA 280	70 rgaaaaccaact 111   1 sgaagcttctgcc 350	130 TGGCAT       AGAAGTGGTGAGA 420 4	190 3GGAACGAGGGGT 	260 TGAGGGAGGAGGG 11 11 11 GGAAGGAACAGC <sup>1</sup>	0 GAGGAGGGCTG(       ACAGAACATGTT	410 .GGGAGGAGG       TGGAGCAATAGA	480 ATCCTTCCCAG           ATCAGATGAGCAT	550 STITICICIAICC   1   SAGAGIGGIGICA 850	CGGGGCTTTTCCG CGGGGCTTTTCCG 1 1 ATCATGATCACAA 920 930	680 690 CCTTCCAGGAGTC(           CCTTGCTGTTAAA(	0 760 GCTTACTGCAGA(              GATACTTGAAGAA	830
GAGAAACTCCAGG 0 270	50 60 AGGGACNAAAAT         1 TTTGGCCAGTCAG	120 GGAAATCTAGG          TCAAAATTGGG	180 ACCTCTGGGTCTG           CCTTATGTGTGCA 480	250 CAACCCTGGGTC 	320 33 CCTGGGTCTGAGG           AAGCACCTCGAGG	90 400 ACCCTTGGTTTGA         AATTCATGGCTGI	460 470 AGATATTCCTGAA' 	0 CTGGCCTGGACGC       AGAAGACGAAGGC 840	590   600   610   620   630   640   610   620   630   640   610   620   630   640   610   620   630   640   610   620	670 CCCCCAGAGTCAC 	740 75 AGCGGGTCATAGA I   II AACACACTGAGGA	810 820
X 10 20 TTTTTTTTGCNCNTCTCTTA 	30 40 50 60 70 80 90  AACTITATITICIGGATCIAGGGAAAGGGACNAAAATGAAAACCAACTGGTAAGGITGGTCAACNINCC	100 120 130 130 140  ACAAGGGGGCACTGTGTNCAGGGAAAATCTAGGTGGCATTGGACCNCTGGGTCT	50         160         170         180         190         200         210         220           GANGGAAGAGGGCTGGGGACTTGGGGGTTGGGCTTGGACCTCTGACTC         1 <td>230 250 260 290 290 290 290 290 290 290 290 290 29</td> <td>300 350 360 GTCTGANGGAGGAGGAGGAGGAGGAGGGGGGTCTGGACTCCTGGGTCTG  GTCTGANGGAGGAGGTCTGGGTCTGAGGGAGGAGGGGGTCTGGACTCCTGGGTCTG  GTCTGANGGAGGAGCTCTGGGGAGCACTCTGGGGGGGTCTGGAGGTCTGGGTCTGGAGGACACTTTCTATA  AAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATA  600 610 650 660</td> <td>370 380 420 430 430 430 430 430 430 430 430 AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG</td> <td>440       450       460       470       480       490       500         CCTGAGGGGGGGGGGGGGAGGATGTATTTGGGGGGTCAATTTCA       1       2</td> <td>  510   520   540   550   570   TGGGTTTCTCTATCCACTCAGTGAATTTGCAGAGGTTG</td> <td>580       600       610       620       630       640         GTGTAGACACCAACGCCCAACTTGCCCAACGCCCTGCAAGTA         I I I I I I I I I I I I I I I I I I I</td> <td>  650   660   670   680   690   700   710   710   CCCGTTGCAGAGCCCCCCCAGAGTCACGTTGCAGGAGTCCTTCTGGTCTTGCCCTCCGCGGG   1   1   1   1   1   1   1   1   1</td> <td>720 730 740 750 760 770 780 CGCAGAACATGTGGGGTGTACAGAGCTTACTGCAGACCTCCTCAGACACCACCGACACGT</td> <td>800 8</td>	230 250 260 290 290 290 290 290 290 290 290 290 29	300 350 360 GTCTGANGGAGGAGGAGGAGGAGGAGGGGGGTCTGGACTCCTGGGTCTG  GTCTGANGGAGGAGGTCTGGGTCTGAGGGAGGAGGGGGTCTGGACTCCTGGGTCTG  GTCTGANGGAGGAGCTCTGGGGAGCACTCTGGGGGGGTCTGGAGGTCTGGGTCTGGAGGACACTTTCTATA  AAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATA  600 610 650 660	370 380 420 430 430 430 430 430 430 430 430 AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	440       450       460       470       480       490       500         CCTGAGGGGGGGGGGGGGAGGATGTATTTGGGGGGTCAATTTCA       1       2	510   520   540   550   570   TGGGTTTCTCTATCCACTCAGTGAATTTGCAGAGGTTG	580       600       610       620       630       640         GTGTAGACACCAACGCCCAACTTGCCCAACGCCCTGCAAGTA         I I I I I I I I I I I I I I I I I I I	650   660   670   680   690   700   710   710   CCCGTTGCAGAGCCCCCCCAGAGTCACGTTGCAGGAGTCCTTCTGGTCTTGCCCTCCGCGGG   1   1   1   1   1   1   1   1   1	720 730 740 750 760 770 780 CGCAGAACATGTGGGGTGTACAGAGCTTACTGCAGACCTCCTCAGACACCACCGACACGT	800 8
GGAGCCCTTCCG 240	30 AACTTTATTTCT             GCTTATTTATG 310	100 ACAAGGGG 	150 160 GANGGAAGAGGG           CCTGGCTGACTT'	230 TGAAGGAGGAG         1  GCACTGACAAG	300 GTCTGANGGAG 1   AAACTCAGAAA 600	370 AGGGAGGAGGG         CGACTTACAGG	440 CCTGAGGAGG         TCAAAGGACTT 740	510 TGGGTTCCCAG 	580 GTGTAGACAC·       GTGTGACTCCC 890	650 CCCGTTC       CCAGTGAGGA( 960	720 CGCAGAACAT          CAAAAGGGAT	1030

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130 140 150 160 170 180 190
ATCTAGGTGGCATTGGACCNCTGGGTCTGANGGAAGAGGGGCTGGGGACCTNNACCTCTGGGTCTGGGGAACG
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AGGCAAGAGTTCCCCGCGGTAGGCACTGCGAAGCAATGCTGATGCTCCGGATGGTGTCTCAGACTCGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCTCAAGTGAATTTGAATACTGCATTTACAGTGTAGAGTAACATAACATTGTATGCATGGAAACATGG
                                                                                    860 870 880 890 900 910 920 GCACCCACACACACACCCCAGCACCCCAGCACCCAGCAAACG
CACGCACTGCAGCACGGTAGGCATTCTGCCTGGGACGCAGAGCTCTGGGTCAGCCCCCGCGGACTGGGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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US-09-020-747-38 Sequence 38, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1220 1230 1240 1250 X
TTCGTTTCCATGACCAGTGCCGCCTGCCAGGCTGCGGGCTGCC
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298
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630 640 650 660 670 680 690 AGACACAGAGCCCTGCAAGTACCCGTTGCAGGAGTCCTTCTG 490 500 510 520 550 AGGATGTTGGGGGTCAATTTCATGGGTTCCCAGTCCCCAGAGTTAACTGGCCTGGACGTTTTCTCTAT 560 570 580 590 600 610 620 CCACTCAGTGAATTTGCAGAGGTTGGTGTAGACACCTGGCACGCCAACTTGGCCACAGGGGCTTTTCCGAA TTCCNNGGGAATTNACCGGGGTTTTTCCCNTTTGGGGGCCAINCCCCCCCTTTCGGGGTTTTGGGNNTAGGTT 440 450 450 500 70 780 790 800 810 820 830 840 AGACACCACCGACACGTTCTGCCTGGGACGCAGAGCTCTGGGTCAGC 850 860 870 880 890 900 910 CCCCGCGCGACTGGGCAGACCTCCTTGAAGAGGCCAGACACACCCGTGAGCTCACCGTTCGCCAGCAGA 539 NATTNGGGGAANAANCCAAATGTNAAGAAAATTTAACCCATTATNAACTTAAATNCCTNGAAACCCNTGGNT 160 200 210 220 TCCAAAAATTTTTAACCCTTAAATCCCTCCGAAATTGNTAANGGAAAACCAAATTCNCCTAAGGCTNTTTGA 230 240 250 250 GAATTTTINNANGNCCCAAAAAANCCCCCAANAAAAAACTCCCAAGNNTTAATTNGAATNTCCCCCTTCCC 510 520 530 540 550 550 AGGTTHGATTTAAACCCCCTTHANTTHTTTHACCCNNGNCTNAANTATTTHGATTCCGGTGTTTCCTNTT 300 310 320 330 340 0 920 930 940 950 960 970 CCCCAGCCAGAAACGAGGCAAGGCAATGCTGATGCTCCG 239 Significance 274 Mismatches 14. US-09-030-606-173' (1-1265) US-08-806-596-26 Sequence 26, Application US/08806596 Conservative Substitutions Optimized Score AGGCCTTTTGGGAA--580 590 TCCCCGGGNCGGCCG Initial Score Residue Identity Gaps

Significance Mismatches

Optimized Score Matches

57 33%

ACCTGCCCCCCATGGCCGTNCGCNTCCCTGGTCTGNCAAGGGAAGCTCCCTGTTGGAATTNCGGGGANAC 230 240 250 260 270 270 280 290 GAGGAGGAGGAGGAGGGGCTGGGGGCTCTGGACTCTGGGTCTG ----GTCANGGAAACAACANACC 370 380 390 400 410 420 430 440 GGAGGGGCTGGGGCCTGGACTCTGGCCTGAGGG 520 530 540 550 560 570 580 CAGTCCCCAGAGTTAACTGGCCTGGACGTTTTCTCTATCCACTCAGTGAATTTGCAGAGGTTGGTAGAC ACCTGGCACGCCAACTTGGCCACACGGGGCTTTTCCGAAAGACACAAGGCCCT----GCAAGTACCGGTTGC 660 670 680 690 700 710 720 AGATCAGGGGCCCCCCAGAGTCATGCAGTCCTTCTGGTCTTGCCCTCCGCCGGGGCAGAACATGC CTTTACACCCCCTNNTACTCNTCTCCTCTNTTNTCCTGNCNCACTTTTNACCCCNNNATTTCCCTTNAT 580 530 640 300 310 320 330 340 350 . 360 ANGGAGGAGGAGGAGGAGGGGGTCTGGACTCCTGGGTCTGAGGGA 450 460 470 470 480 490 500 510 AGGAGGGCTGGGAACAGATATTCCTTCCGCAGGATGTATTTGGGGGGTCAATTTCATGGGTTCC 730 740 750 760 770 780 790 TGGGGTGGTACAGGGGTTACTGCAGGACCTCCTCAGACACCACCGACACGTTCACGCACTGCA TGATCGGANNCTNGANATTCCACTNNCGCCTNCCNTCNATCNGNAANACNAAANACTNTCTNACCCNGGGGA 650 660 670 710 800 810 820 830 840 850 860 --- GCACGGTAGGCATTCTGCCTGGGACTCTGGGTCAGCCCCCGCGACTGGGCAGGACCTCCT 870 880 890 X 900 910 920 920 TGAAGAGGCAGAGCAGCAGCAGCAGAAAAGAAAAGAGGTT 3' (1-1265) Sequence 18, Application US/08806596 NTGGCCNTNCCCCCCNNNTCCTTNCCC 820

Gaps

CTCCTGGGTCTGANGGAGGGGCTGGACTCCTGGGTCTGAGGGAGGGGGGTCTGGACTCCT CICAGCCAGCTCTCAACATTGGGCATGTCCAGCAGTTCT---CCAAACACGTAGACACCAGNGGCCTCCA 330 340 350. TCAGCTAAGTAGTCAGCATAAGCAAACACTGTG-AGCAGCCGGAAGGTAGAGGCAAAGTACT 220 230 240 250 260 270 90 100 110 140 ACNTNCCACAAGGGGGCA--CTGTGTNCAGGGAAAATCTAGGTGGCATTGGACCNC 150 160 170 180 190 200 210 TGGGTCTGGGTCTGGGGAACGAGGGGGTTGGGGCTTGGACCT 20 30 40 50 50 60 70 30 TCTTAAACTITATTTCTGGATCT - AGGGGAAAGGGACNAAAAATGAAAAACCAAC ccgctggttgcgctggtccagngnagccacgaagcacgtcagcatacacagcctcaatcacaaggtcttcc x 10 50 60 70 x Conservative Substitutions |||| | AGGGTGACAACTGAGAGGT | 150 | 160 X IV TTTTTTTGCNCNTC TGGTAAGGTTGGGTCAA

TCACTTCCGCACTCATCACTGCACTGTGGGGGACTTGGGCTCAGGATGTCCAG 40 450 450 460 470 480 AGACGTGGTTCCGCCCCTCNCTTAATGACACCGNCCANNCAACCGTCGGCTCCGCCGANTGNGTTCGTCG 500 510 520 530 540 550 | || || || || TCTGCCTG

| 580 | 590 | 600 | 610 | 620 | 630 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 620 | 630 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640 | 640

| 650 | 660 | 710 | 710 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 | 720 640

CANCCNCATANGAAGCCNG 790 X

CAGAACATGCTGGGGTGGTACAGCGGGTCATAGAGCTTACTGCAGACCTCCTCAGACACCACCACGACACGTTC

740

US/09020747 16. US-09-030-606-173' (1-1265) US-09-020-747-11 Sequence 111, Application '1.94 496 0 A II Significance Mismatches Optimized Score = 256
Matches = 298
Conservative Substitutions 57 36% 24 Score Identity Initial Residue Gaps

X 10 20 TTTTTTTTGCNCNTCTCTTA 

450 460 470 480 490 500 510
GGCTGGGAACAGATTCCTTCCG-CAGGATGTATTTGGGGGTCAATTTCATGGTTCCCAGTC
III III | II

GGCACGCCĂĂCTTGGCCA---CACGGGGCTTTCCGAAAGACACAAGGCCCTGCAAGTACCCGTTGCAGAT 

							*			
1150 1160 1170 1180 1190 1200 1210 730 740 750 760 770 780 790 TGGGTGTACAGCGGTCATACTGCAGACCTCCTCAGACACCACCGACACGTTCACGCACTGCA	800 810 820 830 840 850 GCACGGTAGGCATTCTGCCTGGGACGCAGGTCTGGGTCAGCCCCCGCGACTG   AAAA X	17. US-09-030-606-173' (1-1265) US-08-850-713-6 Sequence 6, Application US/08850713  Initial Score = 56 Optimized Score = 84 Significance = 1.87  Residue Identity = 42% Matches = 94 Mismatches = 124  Gaps = 4 Conservative Substitutions = 0	140         150         170         180         200         210           NCTGGGTCTGANGGAAGAGGGCTTGGAC           I I I I I I I I I I I I I I I I I I I	220 230 240 250 260 270 280 CTCTGACTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	290 340 350 330 350 350 340 350 350 GACTCCTGGGTCTGAGGGGGCTGGGGGGTCTGGACTC CTGGGTCTGGGGGGTCTGGACTC	360 370 380 390 400 410 420  CTGGGTCTGAGGGGGCTGGGGATCTGTACCCTTGGTTTGAGGAGGGGCTGGGGCCTGGACT	430 440 450 460 CCTGGGCCTGAGGGAGGGGCTGGGAACAGAT	18. US-09-030-606-173' (1-1265) US-09-020-747-13 Sequence 139, Application US/09020747	Initial Score = 55 Optimized Score = 114 Significance = 1.80 Residue Identity = 37% Matches = 140 Mismatches = 226 Gaps = 11 Conservative Substitutions = 0	850 860 870 880 890 X 900 910 CGCGACTGGGCAGACGCCTTGAAGAGGGCAGACACACCCGTGAGCTCACCGTTCGCCAGCAGACCC  CGCGACTGGGCAGAGGCCTCCTTGAAGAGGGCAGCACCACACACCGTTCGCTTCGCAGACCC  GGGAATCTTGGCATC X 10 20

AAGTGT 380

 
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 GCAGAGGACCTCACCGTGAGCTCACCGTTCGCCAGCAGACCCCCA---GCC
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Matches = 189 .
Conservative Substitutions 1110 960 950 38% 13 940 11 0 11 Initial Score Residue Identity Gaps

AAGAGTICCCCGCGGTAGGCACTGCGAAGCAATGCTGATGCTCCGGATGGTGTCAA

920 930 CAGCCAGAAACGAGGC

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CAGAGGACCTCCTTGAAGAGGCAGACACACCGTGAGCTCACCGTTCGCCAGCAGGCCAGCAGCCAGAAAA
                                                                                                             930 940 950 960 970 980 990
CGAGGCAAGGAAGCAAGCAATGCTGATGCTCGGATGGTGTCAGACTCGGACA
                                                                            gaagtccnttcnagggntaaangcccccctnncgg
730 740 x
                                                                                                                                                                                                                                                                   29%
13
                                                                                                                                                                                                                                                                Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                       .000 1010
CGGATTCGTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 840 850 850 ACGITCACCACIGCACITCIGGACGCAGACTCIGGGICAGCCCCCCCCGCACIGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          570 580 590 600 610 620 630
TIGCAGAGGITGGCCACGCCAACTIGGCCACGGGGCTTTCCGAAAGACACAAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --NCCCCGGTTANTNAATCCCC--CNNCCCCAATTATACCGANTTTTTTNGAATTGGGANCCCNCGGGAA 370 380 400 410 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCCCCAGAACATGCTGGGGTGGTACAGCGGGTCATAGAGCTTACTGCAGACCTCCTCAGACACCACCGAC
                                                                                                                                                                                                                                       TTTTTTTTTTTTTTTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                 430 440 450 460 470 490 GGACTCCTGCGGACAGATATTC-CTGAATTCCTTCCGCAGGATATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAACCCCTCCATINAAIGNAAACTTCCGAAATTGTCCAACCCCTCNTCCAAAINNCCNTTTCCGGGNGG
                                                                                                                                                                                                                                                                                                                                       -----NNTTAAATTAAATNTTNNTTGGNGGNNNAA
130 140
                                                                                                                                                                                                                                                                  140 150 160 170 180 x 190 200 GGACCINNACCICIGGGTCTGGGGAACGAGGGGTTGGGGGCT
            1140 1150 1160 1170 1180 1190 1200
GARGIGTAGGAGTICTGGAAACAGTGTGCGGCTGACAGCACCCACTGCGGATGCACCAGGACGCCCGAGCA
                                                                                                                                                          \frac{1.80}{513}
                                                                                                                                                         Significance
Mismatches
                                                                                                                             (1-1265)
Sequence 20, Application US/08904809
                                                                                                                                                          Optimized Score = 206
Matches = 240
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                   GGGTTCCAAACCCAANTTANNTTTGGA-----
                                          55
30%
25
                                                                                                                               20. US-09-030-606-17:
US-08-904-809-20
                                                                                                                                                            Initial Score Residue Identity Gaps
                                                                                              GAACAATTC
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CNGCCCCCCCCCCCTCCANTNNGGGGGACTGCCNANNGCTCCGTTNCTNGNNACCCCCNNNGGGTNCCTCGGTTGTC
380 410 420 430 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   850 860 870 880 890 900 910 CCCCGCGCGACTGGGCAGAGGCTCTTGAAGAGGCCAGCAGACACACCCGTGAGCTCACCGTTTCGCCAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GANTCNACCGNANGCCANGGATTCCNAAGGAAGGTGCGTTNTTGGCCCCT----ACCCTTCGCTNCGGNNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTCCCTGNAGNCNANAAANTGGGCCNCGGNCCCCTTTACCCCTNNACAAGCC--ACNGCCNTCTANCCN 310 350 350 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 780 790 800 810 820 ' 830 840
AGACACCACCGACACGTTCAGCCACTGCAGCACGCTAGGCACGCAGAGCTCTGGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630 640 650 660 670 680 690 AGACACACAGAGTCACCGTTGCAGGAGTCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GICTIGCCCICCGCCGGCGCAGAACAIGCIGGGGTGCTACAGCGGGTCAIAGAGCTIACTGCAGACCICCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560 570 580 590 600 610 620 CCACTCAGTGAATTTGCAGAGGTTGGTGAACACCTGGCACGCCAACTTGGCCACACGGGGGCTTTTCCGAA
                                                                                                                                                                                                                                   AGGANNCNCCCTAAAATCANACTGTGAAGATNATCCTGNNNACGGAANGGTCACCGGNNGATNNTGCTAGGG
90 140 150 150 150 160
                                                                                                                                                                          TTTTTTTTTTANGTGTN X
                                                                                                                                                                                                                                                                                                                                                                             490 500 510 520 530 540 550 AGGATGTATITGGGGGGTTTTCTCTAGTCCCCAGAGTTAACTGGCCTGGACGGTTTTCTCTAT
                                                                                                                                 340 350 360 370 380 390 3 400
GGCIGGGGGGTCIGGACTCIGGGGGGGGGGGGGGGGGGATCTGTACCCITGGTTTGAGGGAGGAGGA
                                                                                                                                                                                                                                                                                                    237 Significance
257 Mismatches
21. US-09-030-606-173' (1-1265)
US-08-806-596-22 Sequence 22, Application US/08806596
                                                        Optimized Score = 237
Matches = 257
Conservative Substitutions
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us-09-030-606-173-inv.res

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510	980 CCGGATGGT( 	1050 GTTGTACTC1 CCCCGCCAGG	20 ACTGTGCAGG        CTNCNTCNGC	1200 CACCAGGACC 	. ວວອ		1.73 1.503	70 AAAACCAACT        AACCACCATA	140 GGACCNCTGC             AGAGTCCTG1	210 TGGACCTCTC       TCG-TCNAAN	280 GGTCTGGACTC 	GACTCCT 	0 CCTGGACTCC
500	920 930 940 950 960 970 980 CCCCAGCCAGAAACGAGGAAGGAAGGAATGCTCCGGATGGTG 11	990 1000 1010 1020 1030 1040 1050  TCAGACTCGGACTCGTCCAACTTGATGAGCATGAGCTTAGCGAGCAAGGGTCTGTTGTACTCT	1100	30	1210		Significance Mismatches	10 20 X 30 40 50 60 70  TTTTTTTTTGCNCNTCTCTTAAACTTTATTTCTGGATCTAGGGGACNAAAATGAAAAACCAACT	80.         90         100         110         120         130         140           GGTAAGGTTGGGTCAACNTNCCACAAGGGGCACTGTGTNCAGGGAAAATCTAGGTGGCATTGGACCNCTGG         1<	150	220         230         240         250         260         270         280           ACTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	90         300         310         320         330         340         350           CTGGGTCTGANGGAGGGGCTCTGGGGGTCTGGACTCCT           1	42 3GCTGGGGG
	960 <sup>.</sup> GCGAAGCAA1 	1030 TCGTTAGCGAC      CCGTCTCANNC	GCTCTTGGTG 	1180 ACAGCACCC!           AGCGNCCNCC	1250 AGGGCTGCGA 	US/08904809		50 GGAAAGGGA( TTGTTCTTG1	120 5GAAAATCT?     CGCGGGATGC 100	190 GGAACGAGGG 	60 GAGGGAGGAGG I I I I I I G-GGCAGTTGC 230	340 sgaggggcrg 	410 AGGGAGGAGG
490	950 TAGGGCACT     NGCCTCNCC'	20 1. GCATGAGGT( CTCCNCCNC	110 GGCTCCCTG(         NCCGCGCNG(	1170 GTGCGGCTG1 	1210 1220 1230 1240 12 CCCGAGCAGAACAATTCGTTTTCCATGACCAGTGCCGCCTGCCAGGGC 	cation	Score - 224 - 250 ve Substitutions	40 GGATCTAGG(        TCCTCAAAG	110 TGTGTNCAG(           TAGTACCAG(	180 TGGGTCTGGG 11	260 CTGGGTCTGA(           AAGCNTCCG-( 231	330 TCTGAGGGA(     GAACTGGGT( 300	400 CTTGGTTTGA
480	940 TCCCCGCGG' 1         GCNCNNCGNI	0 1020 ACTTGATGAGC I GNCGNANCNCT	1090 CCACCATCT   CNCNNTCGC	1160 3GAAACAGT(         CGCCGCTGC( 760	1230 FGACCAGTGO CACNNNACCO 830	5) 37, Appli	Optimized Sc Matches Conservative	30 TTTATTTCT( 	100 AGGGGCAC'        AAGGGGTTC' 80	180 TNNACCTCTG( 111 11 ATGCCCTTTG'	250 CCTCAACCC         CCTCCTCG	320 ACTCCTGGG'            SCTGCAGCG' 290	390 ATCTGTACCO
470	930 AGGCAAGAGT       ANCCGCTCCC	1010 ATTCGTCCAA(         CCTCNCNCG	1080 GGCTGGCCT( 	1150 AGGAGTTCT(   CNNACNAAA( 750	1220 CGTTTTCCA:       CCNCGAGGA( 820	3' (1-1265 Sequence	54 Opt 328 Mat 16 Cor	20 X CTCTTAAAC: GCA:	ONTNCCACA	170 GCTGGGACCTI   	240 GGTTGGGGG     CACANGCAG	310 AGGGCTGGA   1 CAGCCCATTG	380 GGGCTGGGG/
460	CAGAAACGA CAGAAACGA I I I I CGACNANGA	1000 CGGACACGG 	1070 GTACGGAGA       CCACNGGNN 670	1140 CGATGGTGT,      CGCTCAANC	AGACAATTC AGACAATTC I I I I CCANGNNTTC	30-606-17 04-809-37	Score Identity -	10 TTTGCNCNT	TGGGTCAA TTGGGTCAA         CGGGCGCAG	160 GGAAGAGGG        GGCAG	230 AGGAGGAGG   1 TGTATTTTT	300 TGANGGAGG I TCGATNCAN	370 AGGGAGGAG
450	920 CCCCAGCC           CCCTTCCC	990 TCAGACT	1060 GGGTGCC L CCNTCAN 660	1130 CCCAGCC 11 CCANTNN	CCCGAGC,	22. US-09-0: US-08-9	Initial Scor Residue Ider Gaps	TTTTTT	80, GGTAAGGT'             GGTAAAGC	150 GTCTGAN      	220 ACTCTGA         CCACTCG	290 CTGGGTC TAAACTG	360 GGGTCTG

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CGCAGAACATGCTGGGGTACAGCGGTCATAGAGCTTACTGCAGACCTCCTCAGACACCACCGACACGT
NGGCCTTTCCATGGAAGGGCCTGGGGGGAAATCNCCTNANCCCAAACTGCCTCTCAAAGGCCACCTTGCACAC 330 340 350 350 400
                                                                                                                                                                                                                                              570 580 590 600 610 620 630 640 AGAGGTTGGTAGACACTGGCACGCCACACGGGGCTTTTCCGAAAGACACAAGGCCCTGCA
                                                                                                                               500 510 520 530 540 550 560 CAATTTCATGGTTTCCACTCACTGAATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                       TTCCCAAANTTCCCCTNGNTTTGGTNNTTTCTCCTCTNCCCTAAAAATGGTNTTCCCCCCCCCNTANGGCG 740 700 710 720 750 760
```

23. US-09-030-606-173' (1-1265) US-08-806-596-16 Sequence 16, Application US/08806596

1.73 501 0 Initial Score = 54 Optimized Score = 275 Significance = Residue Identity = 36% Matches = 290 Mismatches = 12 Conservative Substitutions =

GCCCCAATTCCAGCTGCCACAC x 10 20 

24. US-09-030-606-173' (1-1265) US-09-020-747-13 Sequence 135, Application US/09020747 Initial Score = 53 Optimized Score = 121 Significance = 1.66
Residue Identity = 36% Matches = 132 Mismatches = 218.

Gaps = 11 Conservative Substitutions = 0

GGGAGAGCGACTCCGAGCGCTCTCCCAGAAGCTGGACTTGGCACTGAAACAGCTGGGACACA 950 1000 , 1010

ccacrecececececececerritarestericaececerereses 790 790 740 740 750 750 760 760 770 770 780 790 800 --TCTGANGGAAGAGGG 30 40 50 60 70 80 90 AACTITATITCIGGATCTAGGGGAAAAGGGACNAAAAATGAAAAACCAACTGGTAAGGTTGGGTCAACNINCC GCIGCTCCTCGTCATCTTCCTGCTCGTGCCAACATCCTGGTCAACTTGCTCATTGCCATGTTCAGTTA 590 600 610 620 620 X 10 20 TTTTTTTTGCNCNTCTCTTA 950 960 970 980 990 X 1000 1010 GETAGGGCACTGCGAAGCAATGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCCAACTTGAT Significance Mismatches 930 100 110 120 130 140 ACAAGGGGCACTGTGTNCAGGGAAAATCTAGGTGGCATTGGACCNCTGGG---3' (1-1265) Sequence 109, Application US/09020747 GTTCCCAAGGATGCAAAGCCTGGTGCTCAACTCCTGGGGGGTCAACTCAGT 350 340 350 Optimized Score = 290
Matches = 326
Conservative Substitutions 1020 1030 1040 GAGCATGAGGTCGTTAGCGAGCAAGGGTC 53 36% 21 25. US-09-030-606-173' US-09-020-747-10 St 170 Initial Score Residue Identity Gaps

| 510 | 520 | 530 | 540 | 550 | 550 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570 | 570

1220 TEMPER 27. US-09-030-606-173' (1-1265) US-09-020-747-17 Sequence 174, Application US/09020747 Initial Score = 52 Optimized Score = 405 Significance = 1.59
Residue Identity = 35% Matches = 453 Mismatches = 808
Gaps = 33 Conservative Substitutions = 0

**ACCTNNACCTCTGGGTCTGGGGAACGAGGGGTTGGGGGCTTGGACCTCTGACTCTGAAGGAGGAGGGGTTGG** 

GTGCTGCAGTGCGTGGTGTGTGTCTGANGAGGTCTGCANTAAGCTCTATGACCGGCTGTACCAC 390 440 450 GGGCCTCAACCCCT--

| 310 | 320 | 330 | 340 | 350 | 360 . | 370 | 360 | 360 | 370 | 360 | 360 | 370 | 360 | 360 | 360 | 370 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 370 | 37

---GGCAGAGGACCTCC CGGTAGGCATTCTGCCTGGGACGCAGAGCTCTGGGTCAGCCCCCGCGACTG---810

**AGAGTTCCCCGCGGTAGGGCACTGCGAAGCAATGCTGATGCTCCGGATGGTGTCAGACTCGGACACGGATTC** 

28. US-09-030-606-173' (1-1265) US-08-806-596-38 Sequence 38, Application US/08806596

8 11 Optimized Score = 200 Significance Matches = 222 Mismatches. Conservative Substitutions '. 51 298 33 Initial Score Residue Identity Gaps

-- NTTTAAATTAAATNTT CCATTTCCGGGGGGGGTTCCAAACCCAAATTAATTTTGGA------100 110 120. AGGCCTTTTGGGAA--580 590 TCCCCGGGNCGGCCG

AGGGGTTGGGGGCTTGGACCTCTGAACTCTGAAGGAGGGGTTGGGGGCCTCAACCCCTGGGTCTGAGGGA

CCATTTCCGGGGGGGTTCCAAACCCAAATTAATTTTGGA-----

110

----NTTTAAATTAAATNTT 140 150

```
CGGGGTTTTTCCCNTTTGGGGGCCAINCCCCCNCTTTCGGGGTTTGGGNNTAGGTT 480 450 490
                                                                   700 710 720 730 740 750 760 GTCTTGCCCTCCTCCTC
                                                                                                --AGGNGGGTTTNTGGGGGCCNGGGANTTCNTTCCCCCNTTNCCNC
600 610 620 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 140 150 160 170 180 190 ATCTAGGTGGGCTTGGGACCTUNACCTCTGGGTCTGGGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACACAAGGCCCTGCAAGTACCCGTTGCAGATCAGGGGCCCCCCAGAGTCACCGTTGCAGGAGTCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              502
                                                                                                                                                                                                                                                                                                                                  CCCCAGCCAGAAACGAGGCAAGAGTTCCCCGCGGTAGGGCACTGCGAAGCAATGCTGATGCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 Significance
222 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     29. US-09-030-606-173' (1-1265)
US-08-904-809-38 Sequence 38, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                         930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                            AGGCCTTTTGGGAA--
580 590
                            TICCNNGGGAATINAC
                                          450
                                                                                                                                                                                                                                                                                                                                                               TCCCCGGGNCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial Score
Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                             710
```

360

350

590         600         610         620         630         640         650         ,           TAGACACCTGGCACACTTGGCCACACGGGGCTTTTCCGAAGGCCCTGCAAGTACCCGTTG         1	660         670         680         700         720           CAGATCAGGGCCCCCCAGAGTCACGTTGCAGGAGTCCTTCTGGTCTTGCCCTCCGCCGGCGCAGAACATG         1	730 740 750 760 770 780 790  CTGGGGTGATACAGCGTTACTGCAGACCTCCTCAGACACCACCGACACGTTCACGCACTGC  1	800   810   820   830   840   850   860   870   810   810   810   850   860   870	870         880         890         90         910         920         930         940           AAGGGCAGACACACCACCACCACCACCAGCCAGAAACGAGCAAGAGTTCC         1<	950 960 1010  CCGCGGTAGGCACTGCGAATGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCCAACT	1020 1030 1040 1050 1060 1070 1080  TGATGAGCATGAGGAGCAAGGGTCTGTTGTACTCTGGGTGCCGTACGGAGGCTGGCT	X 1090 1100 1110 1120 1130 CCATCTGGCTCCTTGGTCGGCCTCAAGACTGTGCAGGCCCAGCC   C C X
E4 ()	U A	0 5 7	7 0	ന			

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GCGCACTCGCAGG  X 10 20	440         450         460         470         480         490         500           AGGGAGGAGGACGAGGATGTATTTGGGGGTCAATTTCATGGG           1   1   1   1   1   1   1   1   1   1	0         520         530         540         550         560         570         580           TTCCCAGTCTAACTGGGCC-TGGAGGTTTTTTTTTTCTCAGTGATTGGGGTTGGTG	590   600   610   620   630   640   650	660         670         680         690         710         720           TGCAGATCAGGAGTCCTTCTGGTCTTGCCGCGGCGCAGAACA           1111	730 740 750 760 770 780 790  TGCTGGGGTGCTACAGCGGTTACTGCAGACCTCCTCAGACCACCGACACGTTCACGCACT	810   820   830   840   850   860	870   880   890   900   910   920   930	40 950 960 970 980 990 1000 1010. CCCCGCGCGTAGGCCACTGCGAATGCTCCGGATGCTCCGGATCCGCACGGATTCGTCCAA	1020 1030 1040 1050 1060 1070  CTTGATGAGCATGAGCTTAGCGAGCAAGGGTCTGTTGTACTCTGGGTGCCGTACGGAGGCTGGC	1100	1160	1230 1240 1250 1260 X CATGACCAGTCCGGGCTGCGGGCTGCC
	440 450 AGGAGGAGGGCTGGGA	510 520 TTCCCAGTCCCCAGAGTT	590 TAGACACCIGGCACGCCA	660 TGCAGATCAGGGGCCCCC              TGCTCATCAAGTTGGACG	740 TGCTGGGGTGGTACAGCG I I I I I C CTACCGCGGGGAC-TCT	800 GCAGCACGGTAGGCATTC 	870 880 TGAAGAGGCAGACACAC                   TCCAGTGCAAGGACGTCC 460 470	940 CCCGCGGTAGGCACTG       TGATCAACTAGCCAGCAC 530 540	1020 10 CTTGATGAGCATGAGGTC 	1080 1090 1 CTCCACCATCTGGCTCCC 	1160 CTGGAAACAGTGTGCGGC 	1240 CATGACCAGTGCCGCCTG

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| 1130 | 1080 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 1130 | 
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560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 | 560 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTTTGAAAGATCGTGTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 870 880 890 900 910 920 GGCAGAGGACCTCCTTGAAGAGGGCAGACACACCCGTGAGCTCACCGTTCGCCAGCAGACCCCAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.45
870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 Significance
137 Mismatches
860
                                                                                                                                                                                                                                                                                                                                                                                             33. US-09-030-606-173' (1-1265)
US-09-020-747-13 Sequence 131, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34. US-09-030-606-173' (1-1265)
US-08-806-596-40 Sequence 40, Application US/08806596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score = 116
Matches = 137
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1220 1230
CAATTCGTTTCCATGACCAGTGCCGC
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38%
27
                                                                                                                               CCAAAGCCTTTAAATCCCTC
880 890
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670

099

640

 CTTGGCCAAATACTCAGCGTAG

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1150 1160 1170 1180 1190 1200 1210
TAGGAGIICTGGAAACAGIGGGGGIGACAGCACCCACTGCGGATGCACCAGGACGCCCGAGCAGAAAT
                                                                                                                                                                                                                                                                                                                                            CTTGGCCAAATACTCAGCGTAG
                                                                                                                                                                                                                                                                                                                         930 940 950 960 970 980 990
AGGCAAGAGTTCCCCGCGGTAGGCACTGCGAATGCTGATGCTCCGGATGGTGTCAGACTCGGACACG
                                                            AAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGCTCTGTTAGCCCCATG 30 8.0 8.0 90
                                    1080 1090 1100 1110 1120 1130 1140 AGGCTGGCCTCAAGACTGTGCAGGCCCAGCCCGATGGTG
                                                                                                                                                                                                                                                                         Significance
Mismatches
                                                                                                                                                                                                                                         US-09-030-606-173' (1-1265)
US-09-525-397-6 Sequence 6, Application US/09525397
                                                                                                                                                                                                                                                                            40% Matches - 76
6 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgcrgcrgaggrgcgrantgcacaggcrgcrg rgcrgcrgaggrgcrg 180 x
                                                                                                                                                     TGCTGCTGAGGTGCGTANTGCACAGCTGGGGGGCTG
                                                                                                                                                                                                                                                                                     11 II II
                                                                                                                                                                                               1220
TCGTTTTCCATGA
                                                                                                                                                                                                                                                                                   Initial Score
Residue Identity
Gaps
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37. US-09-030-606-173' (1-1265) US-09-841-894A-6 Sequence 6, Application US/09841894A

TCGTTTTCCATGA

Initial Score = 49 Optimized Score = 76 Significance = 1.38
Residue Identity = 40% Matches = 82 Mismatches = 113
Gaps = 6 Conservative Substitutions = 0
930 940 950 960 970 980 990
AGCAAGAGTTCCCCGCGGTAGGCACTGCGAAGCAATGCTCGATGCTCCGGATGGTCTAGACTCGGACCG
AGCCAAGAGTTCCCCGCGGTAGGCACTGCGAAGCAATGCTCGATGCTCAGACTCAGACTCGGACCGTAGCCTAGCCTAG

us-09-030-606-173-inv.res

| 10 | 350 | 360 | 370 | 380 | 390 | 400 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | 410 | Trestacecaaataeceaagagaeaersaagagataetaagagaeagagaeageetgataaeeaageetgeea

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1150 1160 1170 1180 1190 1200 1210

TAGGAGTTCTGGAAACAGTGCGGCTGACACCCACTGCGGATGCACCAGGACGCCCGAGCAGAACAAT
                                                                                                                                                                                                                                                                                                                                                                                          GACAGCTTCAGCCGCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 210 220 230 240 x 250 260 GGTTGGGGGGCCTCAACCCCTGGGTCTGAGGGGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCTGCCAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCA 100 110 120 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 280 290 300 310 320 330
GGGCTGGGGGTCTGGGTCTGANGGA-GGAGGGGCTGGACTCCTGGGTCTGAGGGAGGGGG
                                                                                                                                                                                                                                           = 1.31
= 155
= 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 500 510 520 530 540 GGATGTATTTGGGGGTCAATTTCATGGGTTCCCAGTCCCCAGAGTTAACTGGCCTGGACGTTTTCT
                                                                                                                                                                                                                                           Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Significance
Mismatches
                                                                                                                                                                                                    '3' (1-1265)
Sequence 3, Application US/09071710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13' (1-1265)
Sequence 3, Application US/09525397
                                                                                                                                                                                                                                        Optimized Score = 89
Matches = 98
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimized Score = 89
Matches = 98
Conservative Substitutions
                                                                                              48
38%
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38%
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US-09-071-710-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39. US-09-030-606-17
US-09-525-397-3
                                                                                                                                                                                                                                       Initial Score Residue Identity Gaps
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Residue Identity
                                                                                                                                                   1220
TCGTTTTCCATGA
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GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTACCACCGGGAGAAGCAGGTG 30 40 50 50 60 70 80 90
                                                                                                                                                                                                                                                                                  TTCCTGCCCAAATACCGAGGGACACTGGAGGACAGCCTGATGACCAGCTTCCTGCCA 110 110 120 130 140 150 150
                                                                                                                                                                                                                                                        GACAGCTTCAGCCGCCTCACC
                                                                                           200 210 220 230 240 x 250 260 GGTTGGGGGCCTTGGACCCTCTGAAGGAGGAGGGTTGGGGGCCTCAACCCCTGGGTCTGAGGAGGA
                                                                                                                                GACAGCITCAGCGGCCTCACC x 10 20
                                                                                                                                                                         420 430 440 450 460 470 480 GGCTGGGGGCTGGGGACAGATATTCCTGAATTTCCTTCGCA
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155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Significance
Mismatches
                                       Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41. US-09-030-606-173' (1-1265)
US-09-841-894A-3 Sequence 3, Application US/09841894A
...40. US-09-030-606-173' (1-1265)
US-08-850-713-4 Sequence 4, Application US/08850713
                                      Optimized Score = 89
Matches = 98
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score = 89
Matches = 98
Conservative Substitutions
                                     48
38%
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38*
2
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                                         0 4 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 0 0
                                   Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Score
Residue Identity
Gaps
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GACAGCTTCAGCCGCCTCACC X 10

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        20
        240
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        260
        270
        280
        290

        CTGAAGGAGGAGGGGTTGGGGCTCAACCCCTGGGTCTGGACTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCGAATTGGGACCGCTGGCTT X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 160 170 180 190 200 210
TGANGGAAGAGGGGCTGGGACCTUTGGGTCTGGGGAACGAGGGGTTGGGGGCTTGGACCTCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trecresceanaraceandededecres de la company d
GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACGGCCTCCTCTACCACCGGGAGAAGCAGGTG 30 40 50 50 60 70 80
                                                                                                                                                                      340 350 360 370 380 390 400 410 CIGGGGGTCIGGACCCTIGGITIGAGGGAGGAGGGCTIGGGATCIGIACCCTIGGITIGAGGGAGGAGGGGATCIGIACCCTIGGITIGAGGGAGGAGGGGATCIGIACCCTIGGITIGAGGGAGGAGGGGATCIGIACCCTIGGITIGAGGGAGGAGGAGGGAACGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 500 510 520 530 540 GGATGTATTIGGGGGGTCAATTTCATGGGTTCCCAGTCCCCAGAGTTAACTGGCCTGGACGGTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 157 Significance
Matches = 165 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13' (1-1265)
Sequence 83, Application US/09020747
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338
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US-09-020-747-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220
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.30 440 450 460 470 480 490 500
CTGGGCCTGAGGGGGCTGGGAACAGATATTCCTGAATTCCTTCGCGCAGGATGTATTTGGGGGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 520 530 540 550 560 570 TITCATGGGTTCCCAGTCCCAGTGAATTTGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAAAAAGCTGTCAAATAGGTGTGACCCTACTAATAATTATTAGAAATACATTTAAAAAACATCGAGTACCTC 320 330 340 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAATCTCCAGCAAGCATCTCATTTAAATAAAGGTTTGTCATCTTTAAAAATACAGGAATATGTGACTTTT 220 230 230 240 250 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 340 350 320 330 340 350 ACTCCTGGGTCTGAGGAGGGGGCTGGGGGGTCTGGACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 \hspace{10mm} 160 \hspace{10mm} 170 \hspace{10mm} 180 \hspace{10mm} 200 \hspace{10mm} 210 \\ \texttt{GTCTGANGGAAGAGGGGCTGGGACTNNACCTCTG----GGTCTGGGGGAACGAGGGGTTGGGGGCTTGGACC}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \frac{1.31}{381}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 90 100 110 120 130 140
GGTAAGGTTGGGTCAACNTNCCACAAGGGGGCACTGTGTNCAGGGAAAATCTAGGTGGCATTGGACCNCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATATGTAAAGAAAGAAATCACACATTAATAATGGTAAGATTGGTTTATGTGATTTTAGTGGTATTTTGG
110 120 130 140 140
                                                                                                                                                                                                                                                                                                                                                                                                                      X 10 20 30 40 50 60 70 TITITITITITICCUCNTCTTAAACTTTATTTCTGGATCTAGGGGAAAGGGACNAAAAATGAAAAACCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 Significance
148 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44. US-09-030-606-173' (1-1265)
US-09-020-747-71 Sequence 71, Application US/09020747
                                                                                                                                       3' (1-1265)
Sequence 71, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Optimized Score = 144
Matches = 148
Conservative Substitutions
                                                                                                                                                                                                                                                                  Optimized Score = 144
Matches = 148
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATATAAGGCTGTAAAATGAAGAATTCTGCC
510 520 530 X
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278
4
                                                                                                                                                                                                                                                                            48
278
4
                                                                                                                                                              US-09-030-606-173'
US-08-904-809-71 St
650 660
GTTGCAGATCAGGGGCCC
                                                                                                                                                                                                                                                                                         Initial Score Residue Identity =
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Residue Identity
Gaps
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  290 300 310 320 330 340 350 address and act of the control of the

580 GGTTGGTG

45. US-09-030-606-173' (1-1265) US-08-904-809-16 Sequence 16, Application US/08904809 Initial Score = 48 Optimized Score = 275 Significance = 1.31
Residue Identity = 36% Matches = 290 Mismatches = 501
Gaps = 12 Conservative Substitutions = 0

260

  46. US-09-030-606-173' (1-1265) US-09-020-747-16 Sequence 16, Application US/09020747 Initial Score = 48 Optimized Score = 275 Significance = 1.31
Residue Identity = 36% Matches = 290 Mismatches = 501
Gaps = 12 Conservative Substitutions = 0

   47. US-09-030-606-173' (1-1265) US-09-020-747-22 Sequence 22, Application US/09020747

Initial Score = 48 Optimized Score = 239 Significance = 1.31
Residue Identity = 31% Matches = 269 Mismatches = 564
Gaps = 16 Conservative Substitutions = 0

| 510 | 520 | 530 | 540 | 550 | 560 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800 | 800

| 850 | 860 | 870 | 880 | 890 | 900 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910

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CCTCTTCCAGCCTCACTTGAGTCCTTGGGGGTTGATAGGAANTNTCTCTTGGCTTTCTCAATAAAATC.
320 330 340 350 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 240 250 260 270 280 290 AGGAGGGGGTTGGGGGCTCCTGGGTCTGGGTCTGGGTCTGGGTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 100 | 310 | 320 | 340 | 350 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNACCTCTGGGTCTGGGGAACGAGGGGTTGGGGGCTTGGACTCTGAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           ' (1-1265)
Sequence 80, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158
167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches = 167
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score
                                                          CAGAGACACONNACCCCGCCNNCANGCGG
RTCCNCGAGGACACNNNACCCCGCCNNCANGCGG
830 840 X
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358
6
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US-09-020-747-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 170
AGAGGGCTGGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial Score Residue Identity Gaps
                                                                                                                                                                                                                                                        1000
CGGACACGGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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CCTGGGACGCAGAGCTCTGGGTCAGCCCCCGCGACTGGGCAGAGGACCTCCTTGAAGAGG3CAGACACACAC 

830

**AAGCAATGCTGATGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCCAACTTGATGAGCATGAGGTCGT** 

1000

1040 X 1090 1070 1080 1090 TAGCGAGCAAGGGTCTCTTGGGTGCCGTACGGAGAGGCTCCACCATCTGGCTCC CCAACNNAATCCNCT 1.24 481 0 Significance Mismatches 49. US-09-030-606-173' (1-1265) US-08-806-596-19 Sequence 19, Application US/08806596 Optimized Score = 211
Matches = 250
Conservative Substitutions 47 328 27

Initial Score Residue Identity Gaps

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-TCTTTATNGGAGGGGGGGGGACACATCNTGACCCCAACTCCCCNCCNCANTGCAGAGAGAGACTCT 110 110 150 140 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 250 250 260 270 280 280 310 GGGCTCGACCTCCTGGGTCTGAMGGAGGAGGGGCTCGGGGTCTGGACTCTGAMGGAGGGGCTCGGGGCTCTGGACTCTGAMGGAGGGGGCTCGGGGGTCTGGACTCTGAMGGAGGGGGCT
                                            CNAAGCTTCCAGGTNACGGGCC
                                                                                                                                320 330 340 350 360 360 380 TGGACTCCTGGGTCTGAGGGAGGGGCCTGGGG
                                                                                                                                                                                                                                                                          390 400 410 450 450 ATCTGTACCCTTGGTTTGAGGGAGGAGGGCCTGGGCCTGGACTCCTGGGCCTTGAGGAGGAGGGCTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                          460 470 480 490 500 510 520 AACAGATATTCCTGCAGTCCCCAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCGGGGCTGGCCACGCNCATCCNTCNAGT-----GCTGNAAAGCCCCNNCCTGTCTACTTGTTTGGAG
230 230 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACNGCNNNGACATGCCCAGNGTTANATAACNGGCNGAGAGTNANTTTGCCTCCCTTCCGGCTGCGCANC 360 310 330 340 350 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              680 690 700 710 720 730 740 GAGTCACCGTTGCAGGCGCGCGCGCGCGCGCGGGGTGCTGGGTACAGCGGG
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CAGGAAGGTGACTGGTGTTGTCATGGAGATCTGAGCCCGGCAGAAGTTTTGCTGTCCAACAAATCTACTG
CAGGAAGGTGACTGGTGTTGTCATGGAGATCTGAGCCCGGCAGAAGTTTTGCTGTCCAACAATCTACTG
CAGGAAGGTGACTGGTGTTGTCATGAGATCTAAAGTTTTGCTGTCCAACAAATCTACTG
A80 480 510 510 520 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600 610 620 630 640 650 660 GCACGCCAACACACAAGACCCTGCAAGTACCCGTTGCAGATCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGITGATGICGAACICNIGGAAAGGGAIACAAIIGGCAICCAGCIGGIIGG---1GI
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTITATIANTECTGGGTTCTTGTCTGGGTTCAAGAGGATGTCGCGGATGAATTCCCATAAGTGAGTCCCTC 330 330 330 380 390
                                                                                                                                                                                                                                                       170 180 190 200 210 220 230 ACTINIACCTCTGGGTTGGGGGGTTGGGGGGTTGGACTCTGACTCTGAAGGAGGAGGGGTTGG
                                                                                                                                                                                                                                                                                                                 100 110 120 130 140 150 160 ACAAGGGGGCACTGGGTCTGANGGAAGAGGGGCTGGG
                                                                                                                                                                                                                                                                                 x 10 20
TTTTTTTTGCNCNTCTCTTA
                                                                                       1.24
465
                          Significance
Mismatches
(1-1265)
Sequence 44, Application US/08904809
                           Optimized Score = 253
Matches = 289.
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                         410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCAAAGGTGCTCG
                                                                                                                                                                                                                     CCAGAATTTCTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGATCTGTACCCT
 50. US-09-030-606-17
US-08-904-809-44
                                Initial Score = Residue Identity = Cans
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750 760 770 780 790 X 800 810 ATAGAGGTTCAGGCACTGCAGCACGCACTCTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAACAANAANTCCCTTCTTTA
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        1020
        1030

        AGCAATGCTGCTCCGGATGCTCCGGACACGGATTCGTCCAACTTGAGGATGAGGTCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAACAANAANTCCCTTCTTTA
X .
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134 Significance
150 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Optimized Score = 134 Significance
Matches = 150 Mismatches:
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1180 1190 1200 1210 1230 1230 CACCCACGGAGCAGCAGCAGCAGCAGTTTTCCATGACCA.
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Sequence 65, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                     s' (1-1265)
Sequence 65, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 134
Matches = 150
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score
Matches
                                                                                              46
38%
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38%
12
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US-09-020-747-65 St
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-030-606-173'
US-08-904-809-65 St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score = Residue Identity = Gaps = =
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                                                                                                                                                                                                                                                                                         810
GCATTCTGCCT
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 GCATGT

53. US-09-030-606-173' (1-1265) US-08-904-809-18 Sequence 18, Application US/08904809 Initial Score = 46 Optimized Score = 246 Significance = 1.1 Residue Identity = 33% Matches = 275 Mismatches = 52 Gaps = 13 Conservative Substitutions = 130 Conservative Substitutions

| 80 | 90 | 100 | 120 | 130 | 140 | 140 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 |

| 650 | 660 | 670 | 680 | 690 | 700 | 710 | TACCGTTGCAGATCACCGTTGCAGAGTCCTTCTGGTCTTGCCCTCGCCGGCG | GOVERNMENT | GOVERNMENT

...54. US-09-030-606-173' (1-1265) US-08-904-809-23 Sequence 23, Application US/08904809

Initial Score = 46 Optimized Score = 233 Significance = 1.18
Residue Identity = 29% Matches = 260 Mismatches; = 611
Gaps = 22 Conservative Substitutions = 0

220	620 630 640 650 660 670 680  GGCTTTTCCGAAAGACACAAGGCCCTGCAAGTACCCGTTGCAGATCAGGGCCCCCCAGAGTCACCGTTGC
210	670 SCCCCCAGAG      ACCCTNGINC
200	660 LAGATCAGGGG      NAGCTGTCNNA
190,	650 STACCGTTGC       PACNTCTTCN 260
180	640 GCCCTGCAAG        CTNCCNACCCT
170	630 AAAGACACAAK       CCAGCNTCNCC
160	620 GGGCTTTTCCG/ 

.260 X GGCTGCC | 11 TCTTTCC 870 X 55. US-09-030-606-173' (1-1265) US-09-020-747-10 Sequence 106, Application US/09020747 Initial Score = 45 Optimized Score = 149 Significance = 1.11
Residue Identity = 35% Matches = 170 Mismatches = 294
Gaps = 12 Conservative Substitutions = (

56. US-09-030-606-173' (1-1265) US-08-806-596-2 Sequence 2, Application US/08806596

Initial Score = 45 Optimized Score = 242 Significance = 1.11
Residue Identity = 36% Matches = 29% Mismatches = 47%
Gaps = 36 Conservative Substitutions = 0

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710 720 730 740 750 760 770 TCGGCGGCGCAGAACATGCTGGGGTGGTACAGGGGGTCATAGAGCTTACTGCAGACCTCCTCAGACACCAC
                                                                                                          TGACTCCGGTTCTGACTTTTGAGGAGGTTGTTCATCATGATCACAAGGAACGG 260 270 280 290
                                                                                                                                                                                                                       GAAACGAGGCAAGATTCCCCGGGGTAGGGCACTGCGAAGCAATGCTGATGCTCCGGATGGTGTCAGACTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3' (1-1265)
Sequence 2, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       009
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368
36
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390
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US-08-904-809-2
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ACTCCTGGGCCTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           850
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ATGANTGAGCTAACTCNCATTAATTGCGTTGCGCTCCCCGCTTTCCAGTCGGGAAAACTGTCGTGCCA 590 630 640 650 650 TTGATCCTNGCNCCCGGTCTTCGGCTGCGGGTGACGGTTCACTCCTCAAAAGCGGGTNYNCCGGTTATCCCCA 730 740 750 750 x ACGAGAGGCTGGCCTCCACCATCTGGCT-----CCCTGGCTCTTGGTCGGCCTCAAGACTGTGCAGGCC TACGAGCTGCTGATCAAAGGACTTGGACTTGATGAACTTCCCAATCAGATGAGGATGATTGG 710 720 730 740 750 750 770 TCCGCCGGCGCAGAACATGGGGGTGGTACAGCGGGTCATAGAGCTTACTGCAGACCTCCTCAGACACCAC 640 650 660 670 680 690 700 CCCTGCAAGTACCCGTTGCAGGAGTCCT-TCTGGTCTTGCCC CCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGAC 170 180 190 200 200 GCTCGTTTATCACCAGTGAGGAGCAGGAGGTGAGCCCCGCCTGCACCTCTGCTGTTAAACACCCCAGCC 320 330 340 350 360 360 370 380 TGGGCAGAGGACCTCCTTGAAGAGGGCAGACACACCCGTGAGCTCACCGTTCGCCAGCAGACCCCAGCCA 930 940 950 960 970 980 990 GAAACGAGGCAAGGGAAGCAATGCTCCGGATGGTGTCAGACTCG CAGCCCGATGGTGTAGG---AGTTCTGGAAACAGTGTGCGGCTGACAGCACCCACTGCGGATGC----ACCA 780 790 800 810 810 820 830 840 CGACACGTTCAGGCATTCTGGCACGCAGAGGCTCTGGGTCAGCCCCGCGAA TTGCAGAGGTTGGTGTAGACACCTGG----CACGCCAACTTGGCCACACAGGGGGCTTTTCCGAAAGACACAAGG 1200 1210 1220 1230 1240 1250 X GGACGCCCGAGCAGAATTCGTTTTCCATGACCAGTGCCGCCTGCCAGGGCTGCGAGTGCGGGGCTGCC 11.20 1100 AACNGGGGATACCCNGA 800 810

1.11 478 0

Significance Mismatches

Optimized Score = 242 Matches = 298 Conservative Substitutions

45 368 36

Initial Score = Residue Identity = Gaps = =

58. US-09-030-606-173' (1-1265) US-09-020-747-2 Sequence 2, Application US/09020747

ACAGAAATGTTGGATGGTGGAG

 AACNGGGGATACCCNGA 800 810

59. US-09-030-606-173' (1-1265) US-08-904-809-26 Sequence 26, Application US/08904809 Initial Score = 45 Optimized Score = 239 Significance = 1.11
Residue Identity = 32% Matches = 274 Mismatches = 539
Gaps = 30 Conservative Substitutions = 0

  | 390 | 400 | 410 | 420 | 430 | 440 | 440 | 420 | 430 | 440 | 440 | 420 | 430 | 440 | 440 | 430 | 440 | 440 | 430 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440 | 440

 

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) 820 830 840 840 850 860 TCTGCCTGGGACGCAGAGGACCTCCT
                                                                   TGGGNNCCTCGNTCATCCTCTTTTTTCNCTACCNCCNNTTCTTTGCCTCTCCTTNGATCATCCAACCNTCG
                                                                                                                                                  870 880 890 X 900 910 920 930
TGAAGAGGCAGACACACCCGTGAGCTTCGCCAGCAGAGACCAGAGGCAAGAGTT
                                                                                                                                                                                                                            NTGGCCNTNCCCCCCNNNTCCTTTNCCC 820
                                                                                                   740
800 810
---GCACGGTAGGCAT
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Sequence 165, Application US/09020747 3' (1-1265) 60. US-09-030-606-17 US-09-020-747-16

1.04 118 0 Optimized Score 72
Matches 76
Conservative Substitutions 44 388 1 Initial Score Residue Identity

1260 GGCTGCC

3', (1-1265) 61. US-09-030-606-17 US-09-020-747-16

Sequence 164, Application US/09020747

1.04 298 0 Significance Mismatches Optimized Score = 152
Matches = 166
Conservative Substitutions 44 358 6 Initial Score Residue Identity -

60 650 660 670 X 680 690 GCAAGTACCGGTTGCAGGAGTCCTTC CTTATCACAATGAATGTTCTCC X **AAAGACACAAGGCCCT** 

62. US-09-030-606-173' (1-1265) US-08-904-809-31 Sequence 31, Application US/08904809

457 Optimized Score = 190 Significance Matches = 213 Mismatches Conservative Substitutions 44 308 19 3 1 0 Initial Score Residue Identity Gaps

TTTTTTTTGCNCNTCTCTTA

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250 260 270 280 290 CCCTGGGTCTGAGGGAGGGGCTGGGGTC-----TGGACTCCTGGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               racangegeregegeregegeregenchaaregecerencanareceracea
240 250 260 270
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TTTTTTTTGCNCNTCTCTTA

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                                                                                                                                                                                                          370 380 390 400 410 420 430 440
GGAGGGGCTGGGGATCTGTACCCTTGGTTTGAGGGAGGAGGGGCTGGGGGCCTGGACTCCTGGGCCTGAGGG
                                                                                                                              1.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660 670 x 680 690 700 710 720 caegecccccaeagarcatecttctgccttcgccccccaeagaacatgct
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Mismatches
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Sequence 31, Application US/09020747
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Matches = 213
Conservative Substitutions
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308
19
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GTTGGGGGCCTCAAC
                                                                                                                                                   NTACCCACACCGGAAC
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US-09-020-747-3
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340 350 360 370 380 390 400 GGAGGGCTTGGGGTCTGGGTTTGAGGAGGAGGAGGAGGAGGATCTGTACCTTGGTTTGAGG
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GGAAAATCTAGGTGGCATTGGACCTCTGGGTCTGANGGAAGAGGGGCTGGGACCTNNACCTCTGGGTCTGGG
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10 720 730 740 750 750 760 770 770 780
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ACCIGGCACGCCAACTIGGCCACACGGGGCTTTTCCGAAAGACACACAAGGCCCTGCAAGTACCCGTTGCAGAT
                                                                                                                                                                                                                                            TTGAAAGGCCACGCCGTNCCCNCTCCCCATAGNANNTTTINNCNTCANCTAATGCCCCCCCGGCAACNATC 570 620 590 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 530 540 550 560 570 580 CAGTCCCAGTGAATTTGCAGAGGTTGGTGAAC
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GGAGGGCTGGGGATCTGTTTGAGGGAGGAGGGGGCTGGGGGCCTGGACTCCTGGGCCTGAGGG
ANGGAGGAGGGGCTGGACTCCTGGGTCTGAGGGAGGAGGGGCTGGGGGTCTGGACTCCTGGGTCTGAGGGA
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Mismatches
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US-08-806-596-8 Sequence 8, Application US/08806596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimized Score = 253
Matches = 305
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
358
53
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Residue Identity =
Gaps
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us-09-030-606-173-inv.res

CCTCCTCAGACACCACCGACACGTTCACGCACTGCAGCACGGTAGGCATTCTGCCTGGGACGCAGAGCTCTG ATNNCGCCTTGGCCTT

CAGCAGACCCCAGAAAACGAGGCAAGAGTTCCCCGCGGTAGGGCACTGCGAAGCAATGCTGATGCTCCG NTTNGGNNCNNTGCCCCTTTCCCTCTNGGGANNCG 770 780 790 X

GATGGTGTCAGACT

65. US-09-030-606-173' (1-1265)
US-08-806-596-27 Sequence 27, Application US/08806596

Optimized Score = 234 Significance Matches = 266 Mismatches Conservative Substitutions 42 318 23 Initial Score Residue Identity Gaps

CCNNTNNCTCTTCNNGTNTCGNAANGNTCNCNTNTNNNNNNGNCNNGNTNNTNCNT---------CCCTCTCNCN 660 670 680 680 700 700 820 830 840 880 recepçes 850 860 870 880 recepçes accepted accepte

CGAAGCAATGCTGATGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCGACTTGATGAGCATGAGGTC

NATTAAGGCCTCCNNTCTCCGGCCNC 800 810 X

66. US-09-030-606-173' (1-1265) US-08-904-809-27 Sequence 27, Application US/08904809

0.905331Significance Mismatches

Gaps

ACTTGATGAGCATGAGGTCGTTAGCGAGGATCTGTTGTACTCTGGGTGCCGTACGGAGAGGCTGGCC CTGCAGCACGGTAGGCATTCTGCCTGGGACGCAGAGCTCTGGGTCAGCCCCGCGCACTGGGCAGAGGACCTC 870 880 890 900 910 920 930 CTTGAAGAGGCAAGACACACCCGTGAGCTCACCGTTCGCCAGCAGACCCCAGCAGAAACGAGGCAAGAG NNNNAACCNGCTTNCCNTCNTCTCCCNTANCCGCCNGGAANCCTCCTTTGCCTNACCANGGGCCNNNA
500 510 520 530 540 ----GGGGCUNGGTNNCTNCNCTGNTNNCCCNCTCCTCGTC-CCN 620 620 630 1090 1100 1110 1120 1130 1140 1150 rccaccatcagectcctagectctagectctagectctagecttcaagactgtgcagecccagecccaatgattc NTGGNCTGTNCTGTCNNACTTTAATGGGCCNGA-----CCGGCTAATCCCTCCCTCCCTTCCANTTC 430 440 450 460 460 NCNNCGCNNNGCANNTICNCNGTCCCNNTNNCTCTTCNNCTNTCGNAANGNTCNCNTNTNNNNNGNCNNG--- 640 650 660 670 670 GCGGTGATTCAGCCCTGCCCAACCTGATTCTGATGACTGCGGATGCTGTGACGGACCCAAGGGGCAA----A 90 110 110 120 130 140 150 CCCCAGAGTCACGTTGCAGGAGTCTTTCTGGTCTTGCCCTCCGCCGGCGCAGAAC 370 380 390 400 410 420 430 CTGAGGGAGGAGGAGGGGCCTGGACTCCTGGG ---crcreseccaasaarcrcrrsrrrcrccsascccassca 50 60 70 80 rcredergardeccrerrecre Conservative Substitutions 46 CTCAGGACCTCTGACTG---30 40 CCGCCCNTNNCTNGG--GAGCTCTGGGCTGGGT 230 TTGCAGATCAGGGGCC Crescricification cresco 290

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520 530 540 550 560 570 580 TCCCAGTCCCCCAGTCCAGTGAAT--TIGCAGAGGTTGGTG
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100 110 120 120 130 140 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1060 1070 1080 1090 1100 1120 TCTGGGTGCCGTACGGAGAGGCTGGCCTCCACCATCTGGCTCCTTGGTCGGCCTCAAGACTGTGC
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100 110 120 120 130 140 150
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AGGCCCAGCCCGATGGTGTAGGAGTTCTGGAAACAGTGTGCGGCTGACAGCACCCACTGCGGATGCACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990 1000 1010 1020 1030 1040 1050
GTGTCAGACTCGGACACGGATTCGTCGATGAGGTCGTTAGCGAGCAAGGGTCTGTTGTAC
1160 1170 1180 1190 1200 1210 1220
TGGAAACAGTGCGGCTGACGCACCCACTGCGGATGCACCAGGACGCCCGAGCAGAACAATTCGTTTTCC
                                                                                                                                                                                                                                                         Optimized Score = 73 Significance = Matches = 72 Mismatches = Conservative Substitutions =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 Significance
128 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68. US-09-030-606-173' (1-1265)
US-09-020-747-14 Sequence 146, Application US/09020747
                                                                                                                                                                                                       US-09-030-606-173' (1-1265)
US-09-020-747-15 Sequence 151, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimized Score = 113
Matches = 128
Conservative Substitutions
                                            NTCTNCNCNGCCCCNNCCCCCNGNATTAAGGCCTCCNNTCTCCGGCCNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACTGTCTACGAGGTGCATCCGGCTCAGT 170 180 x
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        AGGGAGGAGGAGGAGGAGGAGGAGGACTCCTGGGTCTGAGGGA
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Mismatches
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US-08-904-809-8 Sequence 8, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                      253
305
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Matches
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AGGATTGAAGGTCINTINIAC
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                                                                                                   TGTCGGACTGTTCANCCACCAACTCTACAAGTTGCTGTCTTCCACTGTCTGTAAGCNTNTTAACCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCAGCCCGATGGTGTAGGAGTTCTGGAAACAGT---GTGCGGCTGACAGCACCCACCCACTGCGGATGCACAG
                                                                                                                                                                                                                                                     840 850 860 870 880 890 900 GGTCAGCCCCCCCGCGACTCACGTTCGC
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                 10 700 710 720 730 740 750 760 CETTCTGGTCTTGGTCTTGGTCTTGGTCATAGAGCTTACTGCAGA
                                                                                                                                                                                                                                                                                     ACCCCAGCCAGAAACGAGGCAAGAGTTCCCCGCGGTAGGGCACTGCGAAGCAATGCTGTGTGCTCCGGATGGT
CCGAAAGACACAAGGCCCTGCAAGTACCCGTTGCAGATCAGGGGCCCCCCAGAGTCA - - CCGTTGCAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.76
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US-09-020-747-90 Sequence 90, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 Optimized Score = 122
33% Matches = 142
24 Conservative Substitutions
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GATGGTGTCAGACT
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Total Elapsed 00:00:01.00

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US-09-020-747-17 8
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                                                                                                                           Results of the initial comparison of US-09-030-606-174 (1-1459) with:
    File: 6130043.seq
    File: 6252047.seq
    File: US08806596.seq
    File: US08850713.seq
    File: US08904809.seq
    File: US08904809.seq
    File: US08904809.seq
    File: US09841894A:seq
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Scores

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Matches = 1459 Mismatches
Conservative Substitutions
                                                                              Init. Opt
Length Score Sco:
                                                                                                                                                        **** 6 standard deviations above mean ****
17 Sequence 173, Application 1265 524
17 Sequence 171, Application 1248 482
                                                                                                     1459
                                                               query sequence was found:
                                                                                                                                                                                                                                                                                                                                                                                                         1 (1-1459)
Sequence 174, Application US/09020747
                                                                                                     1459
                                                                                                    1. US-09-020-747-17 Sequence 174, Application
                                        nitial score on initial s
189792
410
410
                                         initial
                                                                                                                    The list of other best scores is:
                                        The scores below are sorted by ir
Significance is calculated based
                                                               A 100% identical sequence to the
 residues:
sequences searched:
scores above cutoff
                                                                                      Description
                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                 1459
100%
0
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00

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0 0

150 160 170 180 190 210  CCTTGCTCGCTAACGACCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACCATCCGGAGCA  [	220 230 240 250 260 270 280  TCAGCATTGCTTCGCAGTGCCCTACCGGGGAACTCTTGCCTTCTGGCTGG	90 340 350 360 360 360 360 360 350 340 350 360 360 360 360 360 360 360 360 360 36	370 380 400 410 420 430 CTGCGTCCCAGGCAGAATGCCTACCGTGCTGCGTGTCGGTGGTGTCTGANGAGGTCTGCAN	440       450       470       480       500         TAAGCTCTATGACCCCANCATGTTCTGCGCCGGCGGAGGCCAAGACCAGAAGGACTCCTG         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	510         520         530         540         550         560         570           CAACGIGAGAGGGGAAGGGGAAGGGGAAGGGGGACACACAC	580         630         640           AGGCCCCCATGGCGAGATGCACACACACACACACACTGACAAACTGAGAAACTGAGAGAAACTGAGAGAAACTGAGAGAAACTGAGAGAGA	50         660         710         720           AGAAACAGAAATAAAGAGAAGCAAAGGAAGAGAGAAACAGAAACAGAAACAGAAACAGAGGC         111111111111111111111111111111111111	730 740 750 760 770 780 790  AGAAACACACACACATAGAAATGCAGTTGACCTTCCAACAGGGCGGCTGAGGGCGGTGACCTCCACCCA	800         810         830         840         850         860           ATAGAAAACTTTTAAAAACTCCCAAAAAACCTGACTAGAAATAGCCTACTGTTGACGGGGAGCC           11111111111111111111111111111111111	870         880         890         900         910         920.         930           TACCAATAACATAAATAGCGTTTATGCATTCATGATATACCTTTGTTGGAATTTT	940 950 960 970 980 990 1000  TGATATITCTAAGCTACACAGTTCGTCTGTGAATTTTTTAAATTGTTGCAACTCTCCTAAAATTTTTCTGA
150 160 17 CCTTGCTCGCTAACGACCTCATGCT 	220 230 240 TCAGCATTGCTTCGCAGTGCCCTAC 	310 GTGAGCTCACGGTGTGTGTCTGC( 	370 380 CTGCGTCCCAGGCAGAATGCCTAC 	440 TAAGCTCTATGACCGGTGTACCA                              TAAGCTCTATGACCGGCTGTACCA 440	510 520 520 520 520 520 520 520 520 520 52	580 590 600 AGGCCGCATGCGAGATGCAGAG 	650 660 670 AGAAACAGAAATAAACACAGGAAT	730 740 AGAACACACACATAGAAATGC	810 ATAGAAATCCTCTTATAACTTT 	870 880 TTACCAATAACATAAATAGTCGA: 	940 950 960 TGATATTCTAAGCTACACAGTT                        TGATATTTCTAAGCTACAGGTT 940 950 96

1070

1060

1050

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6.73
454
0
                                                                                                                      1 1 0
                                                                                                                     Significance
Mismatches
                                                                                                             (1-1459)
Sequence 173, Application US/09020747
                                                                                                                     ore = 683 (
= 710 N
Substitutions
                                                                                                                      Score
                                                                                                                     Optimized Scor
Matches
Conservative (
                                                                                                                      524
598
31
                                                                                            US-09-030-606-174
US-09-020-747-17
                                                                                                                      11 11 11
                                                                                                                      Score
Identity
                                                                                                                      Initial
Residue
Gaps
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res.

-030-606-174

1160

1150

1140

1120

1100

3. US-09-030-606-174 (1-1459) US-09-020-747-17 Sequence 171, Application US/09020747 Initial Score = 482 Optimized Score = 597 Significance = 6.16
Residue Identity = 53% Matches = 674 Mismatches = 454
Gaps = 127 Conservative Substitutions = 0

| 1000 | 1020 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | 1030 | CCAGCCCTCCTCAGGCCCAGGAGTCCAGGCCCCCAGCCCTCCTCCAAACCAAGGTACAGATC 810 810 820 830 840 0 840 850 860 870 880 CCTGACTAGAATAAGTGTTGAGGGGGAGCCTTACCAATAACATAAATAGTCG ----CAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAA 650 650 670 680 750 760 770 780 790 800 810 GCAGTTGACCTCCACCAATAGAAAATCCTCTAATAACTT 830 500 610 AGATGGAGAGACACACI || || || AGGTGTCTACAC---960

AAAAAAAAA 1240 x

Sequence 175, Application US/09020747 4. US-09-030-606-1 US-09-020-747-1

x 10 20 GGTCAGCCGCACACTGTTTCCA 5.61 442 0 Significance Mismatches 563 644 Substitutions 11 Optimized Score Matches Conservative Sub 442 528 139 Initial Score = Residue Identity = Gaps =

410

 (1-1459) Sequence 177, Application US/09020747 5. US-09-030-606-17. US-09-020-747-17

4.74 488 0 503 Significance 543 Mismatches Optimized Score = 503 Matches = 543 Conservative Substitutions .379 518 27 Initial Score Residue Identity

X 10 20 GGTCAGCCGCACACTGTTTCCA GGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCGGTGGTGGTTGACCGCACTGTTTCCA
40 80 x 90 100

240

TCGATTTATGCATACGTTTTATGCATTCATGATATACCTTTGTTGGAATTTTTTGATATTTCTAAGCTACAC 910

CAAGTATAAGTGGACTTGTGCATTCAAACCAGGGTTGTTCAAGGGTCAACTGTGTACCCAGAGGGAAACAGT 

US-09-030-606-174 (1-1459) US-08-904-809-45 Sequence 45, Application US/08904809

1.65 Significance Mismatches Initial Score Residue Identity S

Gaps

90 100 110 120 130 X 140 150
GCCAGGGAGCCAGAGTGGTGGAGGCCAGCTTCCGTACGCACCCAGAGTGGTGGAGGCCAGCCTTCCGTACGCCACCCAGAGTGGTGGTGGAGCCTTCTCCGTACGCACCCAGAGCCTTGCTTCGCTAACAGACCCTTGCTTCGCTAA 310 320 340 350 370 TGTGTGTCTGCCTCTTGCCCAGTCGCGGGGGCTGACCCAGAGCTCTGCGTCCCAGGC 90 100 110 120 130 X 140 150
GCCAGGGAGCCAGGAGGCACCCAGGAGTACAACAACAGACCTTGCTCGCTAA
ACAACAGAGCCTTGCTCCGTACGGCACCCAGGAGACCAACAGACCCTTGCTCGCTAA
ACAACAGACCCTTGCTCGCTAA 1.65 2 0 0 ų 1 Significance Mismatches ) 470 480 490 500 SANCATGTTGCGCCGGGGGGGGCAAGACCAGAAGGACTCC (1-1459) Sequence 45, Application US/09020747 Optimized Score = 200 Matches = 232 Conservative Substitutions Substitutions Conservative 154 738 83 74 450 x 460 ccgcrgraccaccca ||||||| ccgcrgr Initial Score = Residue Identity = Gaps AGAATGCCTACCG 7. US-09-030-606-1' US-09-020-747-4 380

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1240 1250 1260 1270 1280 1290 1300 GTTCAAAAATGGTGAAAATCCTGTCTGTACTAAAAATACAAAAGTTAGCTGGATATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANCTGTGAAGGAAAANGAFGGAATTTTNCCCTTCCG-----GCCNNTCCCCTCTTCTTTACACGCCCC 530 540 550 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCACACTATAAACGTTAACGACCNAGATNANCACTGCTTCAAGTGCACCCTTCCTACCTGACNACCAGNG 360 350 380 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1100 1110 1120 1130 1140 1150 1160
ACAGTGACACAGATTCATAGAGGTGAAACAC ---GAAGAGAAACAGGAAAATCAAGACTCTACAAAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 890 | 990 | 940 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        960 970 980 990 1000 1010 1020
TACACAGITCGICIGIGAATITITIAAAIIGCAACICICCIAAAAIITITICIGAIGITIAIIGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 610 620 630 640 650 660 AGATGCAGAGAGAGAGAAACTGAGAGAAACTGAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAATGCCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGGTGTCTGAGGAGGTCTGCAGTAAGCTCTATGAC 160 170 180 190 200
                                                                                                                                                                                                                                                                                                                                                                                  0.59
560
0
                                                                                                                                                                                                                                                                                                                                                                                       Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1010
    450 X 460 470 480 490 500 ccGCTGTACCAGCTCTGCGCGGGGGGCAAGACCAGAAGGACTCCCCGCGGGGGGGCAAGACCAGAAGGACTCCCCGCCGGTACCAGAAGGACTCCCCGCCGGAAGGACTCCCCGCGGAAGGACTCCCCGCGGAAGGACTCCCCGCGGAAGGACTCCCCGCTGT
                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                              218
249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         850
                                                                                                                                                                                                                                                                                                                                                                                                  1
                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           840
                                                                                                                                                                                                                                                                                                                                                                                                  Optimized & Matches
                                                                                                                                                                                                                                                                                                                (1-1459)
                                                                                                                                                                                                                                                                                                                                                                                                     77
30%
15
                                                                                                                                                                                                                                                                                                                       US-09-030-606-174
US-08-904-809-26
                                                                                                                                                                                                                                                                                                                                                                                                              11 11 11
                                                                                                                                                                                                                                                                                                                                                                                                     Initial Score
Residue Identity Egaps
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GGCAGGCGCCT--GTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAATATGGGAGGCAGAG
                                                                                                    GANATTCCACTNNCGCCTNCCNTCNATCNGNAANACNAAANACTNTCTNACCCNGGGGATGGGNNCCTCGNT 670 680 690 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 100 110 140 140 140 130 130 140 AGGGAGCCAGAGGCCAGCCTCCGTACGGCACCCAGAGTACAACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGACTCCGAG 50 60 70 .80 90 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGANCCGCTCTGCTTGCTGCCCCCANGTGGGCCGCCACCCCTGACCTGGCTCCAAACACTGAGCC 250 300 310 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 380 390 400 410 420 430 CTGCGTCCCAGGCAGAATGCCTACCGTGCAGTGCGTGAACGTGCTGGGTGTCTGANGAGGTCTGCAN
                                                                                                                                                                   CATCCTCTTTTTCNCTACCNCCNNTTCTTGCTCTCTTNGATCATCCAACCNTGGCCNTNCCCC 740 750 760 760 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 20 30 40 70 GGTCAGCCGCACACTGTTTCCAGAGTGAGTGCAGAGCTCCTACACCATCGGGCTGGGCCTGCACACTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 160 170 180 190 200 210 CCTTGCTCGCTAACGACCTCATCCTGAATCCGTGTCCGAGTCTGACACCATCCGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 320 330 340 350 360 GIGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGGCTGACCCAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 450 460 470 480 490 500
TAAGCTC-TATGACCCGCTGTACCACCCCANCATGTTCTGCGCGGGGGGGGGAGACGAGAAGGACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCCCCCACCTGGTTGTCTTTGANGTGAGCCCCATGTCCATCTGGGCCACTGTCNGGACCACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                             0.56 \\ 539
                                                                                                                                                                                                                                                                                                                                                                                                                                              . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score = 234 Significance Matches = 256 Mismatches Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                       (1-1459)
equence 8, Application US/08806596
                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            75
318
15
         ČINNTACTČNTCTČCC
190 600
                                                                                                                                                                                                                                                                                                                 CCCNNNTCCTTTNCCC
810 X 820
                                                                                                                                                                                                                                                                                                                                                                                         9. US-09-030-606-174
US-08-806-596-8 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGCCGACCAAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGAGCTCACGGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score Residue Identity Gaps
                                                                                                                                                                                                                                                                       50 X
AAAAAAAAA
                                                                                                                                                                                                                                                                       1450
```

52

510

ACGTGGGAATCGGTGCATAAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGCACGAG 50 60 70 R0 90 800 810 820 830 X 840 850 860 CCCAATAGAAAATCCTCTTATAACTTTTGACTCCCAAAAAACCTGACTAGAAATAGCCTACTGTTGACGGG 10 20 30 40 50 60TCAGCCGCACACTGTTCCAGAAGTGAGTGCAGAGCTCCTACACCATCGGGCTGGGCCTGCACAGTCTTG 150 160 170 180 190 200 210 CCTTGCTCGCTAACGACCTCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCA ATCAAGNCCTGNATCCACTNNTNCTANAACCGGCCNCCNCGCNGTGGAACCCNCCTTNTGTTCCTTTTCNT 40 550 550 560 600 610 CATTICCGGGTTTACTTTCTAAGGAAAGCCGAGCGGAAGCTGCTA
X 10 20 30 40 CGTCTGAAGCGCACGTCC-----CAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACACATCGCGAGTA 120 130 170 180 990 300 310 320 330 340 350 360 GEGAGGTCACGGGGGGGTGTGACCCCAGAGCT TNAGGGTTAATNNCGCCTTGGCCTTNCCANNGTCCTNCNTTTTCCNNTGTTNAAATTGTTANGCNCCCNC 620 620 630 640 680 CNNTCCCNCNNCNNCNANCCGACCCNNANNTTNNANNNCCTGGGGGGTNCCNNCNGATTGACCCNNCCCC 690 700 710 720 750 GCAACGTGAGAGGGGAA----AGGGGAGGGCAGGCGACTCAGGGAAGGGTGGAGAAGGGGAAACAGAAAC CTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGTGCGTGAACGTGTCGGTGGTGTCTGANGAGGTCTGCAN NGGGAGTGTTCTCCTTACAACCACANNATGCCCGGCTCCTCCCGGAAACCANTCCCANCCTGNGAAGG---0.56 Significance Mismatches US-09-030-606-174 (1-1459) US-08-904-809-8 Sequence 8, Application US/08904809 Conservative Substitutions TNTANTTGCNTTNGGGNNCNNTGCCCCTTTCCCTCTNGGGANNCG 760 770 780 790 X 1 1 Optimized Score Matches 870 880 AGCCTTACCAATAACATAG 75 318 15 . . . Initial Score Residue Identity Gaps

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### 870 | 890 | 900 | 910 | 920 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 93
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(1-1459) Sequence 39, Application US/09020747 13. US-09-030-606-174 US-09-020-747-39 8

0.54 Significance Mismatches = 202 = 217 Conservative Substitutions Optimized Score Matches 73 318 6 Initial Score - Residue Identity - Gaps

0

TTTTTTTTTTTTTCTTTGCT X 10 20

CCCAATAGAAAATCCTCTTATAACTTTTGACTCCCCAAAAACCTGACTAGAAATAGCCTACTGTTGACGGGG 800 790

AGCCTTACCAATAACATAAATAGTCGATTTATGCATTTATGCATTCATGATATACCTTTGTTGGAAT 900 890

14. US-09-030-606-174 (1-1459) US-08-904-809-44 Sequence 44, Application US/08904809

NNAA 740

TNTCCTCNNCNANCNCAATTTTCTTTTNNTCACGAACNCGNNCCNNAAAATGNNNNNCNCCTCCNCTNGTCC 670 680 720 .730

0.48 Significance Mismatches 267 300 Conservative Substitutions Optimized Score Matches 69 34% 21 Initial Score Residue Identity Gaps

AACGACATGGGGGGGGAACCACACACACAGGGCTTT----CTTCCCAATTTATATACCATTC

TABO

TABO

GGGGGGAGCTTCATTTTCATCTTCTCCATCCTGGGCTT----CTTCCCAATTTATATACCATTC

100

110

TABO

TABO

GGGGGGGAGCTCCAATTTTTATATACTTTTTATATACTTTTATATACTTTCATT

15. US-09-030-606-174 (1-1459)
US-09-020-747-44 Sequence 44, Application US/09020747
Initial Score = 69 Optimized Score = 267 Significance = 0.48
Residue Identity = 34% Matches = 540

| Secondary | Seco

us-09-030-606-174.res

74 (1-1459) Sequence 5, Application US/08806596 16. US-09-030-606-17 US-08-806-596-5

0.45 277 Significance 313 Mismatches Conservative Substitutions Optimized Score Matches 67 37**8** 14 Initial Score Residue Identity Gaps

TGACAACTAGAGAGAAACTGAGAAACAGAGAAATAAACACAGGAATAAAGAGAAGCAAAGGAAGAGAG 640 630

| B50 | 860 | 870 | 880 | 990 | 910 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810

GTTGCAACTCTCCTAAAATTTTTCTGATGTGTTTATTGAAAAAATCCAAGTATAAGTGGACTTGTGCATTCA 1030

17. US-09-030-606-174 (1-1459) US-08-904-809-5 Sequence 5, Application US/08904809

0.45 514 0 Significance Mismatches, Optimized Score = 277
Matches = 313
Conservative Substitutions Initial Score Residue Identity Gaps

GTGGTGTCTGANGAGGTCTGCANTAAGCTCTATGACCCGCTGTACCACCCCCANCATGTTCTGCGCCGGGGG 

670 640

CCTGAGGGCGGTGACCTCCACCAATAGAAAATCCTCTTATAACTTTTGACTCCCCAAAAACCTGACTAGAA TCTATGCAAATATGTCTAGACACTTTGATTCACTCAGCCCTGACATTCAGTTTTCAAAGTAGGAGACAGGTT 380 430 440

```
450
```

AATTTGAAATNA 830 X 

18. US-09-030-606-174 (1-1459) US-09-020-747-5 Sequence 5, Application US/09020747

0.45 514 Significance Mismatches Optimized Score = 277
Matches = 313
Conservative Substitutions Initial Score Residue Identity = Gaps

TTTTTTTTTTTTACTGATA 340 350 400 AGTCGCGGGGGCTGACCCAGACTCTGCGTCCCAGGCAGAATGCCTACCGTGCAGTGCGTGAACGTGTC

```
70 780 790 800 810 820 830 840 CTIGAGGGGGGGGGGGGCGTGACTACAAAATCCTCTTATAACTTTGACTCCCCAAAAACTGACTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 920 970 980 950 960 960 970 AU 980 970 970 980 970 980 980 AU 980 980 980 AU 980 980 AU 980 980 AU 980 980 AU 980 
                                                                                                                                                                                                                                              700 710 720 730 740 750 760
AAACAGAAACAGAAACATGGAGGGAGGCAGAAAGCACATAGAAATGCAGTTGACCTTCCAACAGGATGGGG
```

1200 1210 1220 1230 1240 1250 1260 GCACTTTGGGAGGCGAGGCAGGTACACTTGAGGTAAGGAGTTCAAGACCAGCCTGGCCAAAATGGTGAA (1-1459) Sequence 170, Application US/09020747 ACCTGGTGGAAAAATAATTTGAAATNA 810 820 x 19. US-09-030-606-174 US-09-020-747-17 S 1270 ATCCT

Optimized Score = 90 Significançe Matches = 100 Mismatches Conservative Substitutions Optimized Score Matches . 61 378 3 H H I Initial Score
Residue Identity =
Gaps

AGGCCGĂCCAAGAGCCĂĞGGAGCCAĞATGGTGGAGĞCCAGCTCTCCĞTACGGCACCACCAGAGTACAAGAGAC

									-	· · · · · · · · · · · · · · · · · · ·			
									:				
120	CGGAGCA          CTTGTCA  190 .	30 TTGGCGAACG         TGGCAGGTG 260		•	0.37 470 0	OCATGGGG	ACCTCCA	860 GACGGGG         GTGGGAC 150	930 TTGGAAT       GGGGACA	1000 TAAAATT 	1070 TTCAAGG   	1140 GGAAAAA 	GGAGGCG
110	CCTTGOTANGACCTCATGTCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCGGAGCA	26 GGGTCTGC   CTAGGGGTC			Significance = Mismatches ==	650 660 710 710 FAGAGAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	720	90         810         820         830         840         850         860           CCCAATAGAAAATCCTCTTATAACTTTTGACGGGGGGGGG	## 870 ### 890   900   910   920   930   9	940 950 960 970 980 990 1000  TITITGATATITCTAAGCIACACAGTICGICTGIGAATITITIAAATIGITGCAACTCICCTAAAAÎT	1010 1020 1030 1040 1050 1060 1060 1060 1060 1070  TTTCTGATGTTTATTGAAAAATCCAAGTATAAGTGGACTTGTGCATTCAAACCAGGTTGTTCAAGG	1080	1200 CCAGCACTTTG
100	190 CGTGTCCGAGTC 	270 STTTCTGGCTC       SCCTTCAAAGC	340 SCCCAGTC	708904809		690 x 700 GGAAGAGAAAC,   I   ACAAGG	770 SCATGGGGCCT   11 SAATTTTCCTC 70	840 3ACTAGAAAT!          SAAACTTAA	910 IGCATTCATGA 	980 TTTAAATTGT7 	1050 IGCATTCAAAC         CCCCAGGCTC 350	1120 3GTGAAACACC           3GTGGCCCACA	1180 1190 1200 GGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCG
90	GGACGAATCC         AGGGGGAGTT	260 CTCTTGCCTCO I NATGANATTG	330 GAGGTCCTCT	ication US,	Score = ve Substitu	680 Gagaagcaaag	760 CCTTCCAACAG                 GCCTGAACAG	830 CCAAAAACCT 	900 ATACGTTTTA 	970 TGTGAATTTT       GGCGTCATACO	1040 AGTGGACTTGT              ACTGACCATGT 340	1110 GATTCATAGA(     GCTGATCCTG( 410	1180 3GTGGCTCAT
. 80	rcarcaagri rcarcaagri 11 1 sagrccrggg	250 CCGCGGGGAA(           ANGAGACGAA) 220	90 300 310 320 330 340 GTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCCAGTC     .   .	(1-1459) Sequence 47, Application US/08904809	Optimized Score = 242 Matches = 283 Conservative Substitutions	670 CAGGAATAAAG	750 ATGCAGTTGAG 1 1 AAAAAACGAGG	840   820   830   840	890 CGATTTATGC           GGCATTACAG 80	960 ACAGTTCGTC           AAAGGAAGGT	1030 TCCAAGTATA             TGGAGGAACA 330	1100 CAGTGACACA       CCCACCCTCT	
70	GACCTCATGC        CACCAGATTG	240 CAGTGCCCTA( I CCAGAGAGGA/ 210	310 GTGTGTCTGC	174 (1-1459) 47 Sequence	61 368 29	660 Gaaataaacac	740 ACACATAGAAA                 AAAGAAGGAAA	810 CTCTTATAAC      CTTGGGGAGG	880 CATAAATAGT   TGACCCTGAG	950 AAGCTAC 	1020 ATTGAAAAAA ATTGAAAAAA I   AGGACGACAG	1090 CAGAGGAAA .      GCTCTGGAAG 390	1160 1 AAGAGGCTGGG
60	GCTCGCTAAC	230 CATTGCTTCG( 11   1 AATGAANGAG( 200	300 GCTCACGGGT	9-030-606-174 8-904-809-47	Score Identity =	650 61 GAGAACAGAG	730 AGAAACACACI I GANAGATTTI	800 ATAGAAAATC   1   1 AAATAATTTT	870 TTACCAATAA(             TTTCTGTAA( 60 1	940 IGATATTTCTI I CTAATCCCAA	1010 FGATGTGTTT:         FCATCCTGG: 310	1080 ACTGTGTACCO 	50 ACTCTACA
-	た (Cですず ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( )	220 TCAG(       CCTG	290 GTGA( I GA X	20. US-09 US-08	Initial Residue Gaps	6. TGAG	720 AGGC) 11 TGGG	790 CCCAU 11 TICAU	AGCC'       ANAA'	TTTT' AAGG( 230	TTTCI       CTCCI	GTCAL         GTCT	TCAAG

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| BYO | B80 | B90 | 910 | 920 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1350 1360 1370 1380 1390 1400 1410 GAGAATTGCTTGAAT -- ATGGGAGGCAGGGTTGAAGTGAGTTGAGATCACACCACTATACTCCAGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAAGGGGCATAATGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       790 840 850 850 860 CCCAATAGAAATGCTTTTGACTCCCCAAAAACCTGACTAGAAATAGCCTACTGTTGACGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCTCATCCCTGGAGGACGACGACCAACTGACCATGTCCCCAGGCTCCTGTGTGCTGGCTCCTG 300 310 320 330 340 340
CCCAGGTTATATICCTGGACATGGCTGAACCTCCTATICCTACTICCGAGATGCCTTGCTCCCTGCAGCCTG 450 450 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         940 950 960 970 980 990 1000 TITITGATATITITAAATIGCAACTCTCCTAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCTGATGTGTTTATTGAAAAATCCAAGTATAAGTGGACTTGTGCATTCAAACCAGGGT--TGTTCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 660 670 680 690 X 700 710
TGAGAGAAACAGAGAAACACAGGAATAAAGAGAAGGAAGAGAAAACAGAAACAGACATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080 1090 1100 1110 11120 1130 1140 GTCAACTGTGTGACACAGAAACAGGGAAACAGGGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.37
470
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21. US-09-030-606-174 (1-1459)
US-09-020-747-47 Sequence 47, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Optimized Score - 242
Matches - 283
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
36%
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Score = Residue Identity = Gaps =
```

22. US-09-030-606-174 (1-1459) US-08-904-809-69 Sequence 69, Application US/08904809 Initial Score = 60 Optimized Score = 184 Significance = 0.30
Residue Identity = 38% Matches = 212 Mismatches = 32,
Gaps = 18 Conservative Substitutions

| 80 | 100 | 110 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |

| 350 | 350 | 350 | 350 | 360 | 360 | 350 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360

430

420

 23. US-09-030-606-174 (1-1459) US-09-020-747-69 Sequence 69, Application US/09020747 Initial Score = 60 Optimized Score = 184 Significance, = 0.36
Residue Identity = 38% Matches = 212 Mismatches = 324
Gaps = 18 Conservative Substitutions

  | 350 | 350 | 360 | 360 | 340 | 350 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360

Thu May

24. US-09-030-606-174 (1-1459) US-09-020-747-10 Sequence 109, Application US/09020747 Initial Score = 59 Optimized Score = 478 Significance = 0.34 Residue Identity = 36% Matches = 546 Mismatches = 891 Gaps = 59 Conservative Substitutions = 0

 (1-1459) Sequence 17, Application US/08806596 25. US-09-030-606-174 US-08-806-596-17

vpulmized Score = 240 Significance
Matches = 262 Mismatches
Conservative Substitutions 34% 15 Initial Score = Residue Identity =

7AAGCTCTATGACCCGCTGTACCACCCCANCATGTTCTGCGCCGGCGGAGGGCAAGACCAGAAGGACTCTG 

730 X 770 X 790 AGAAACACACACATAGAAATGCAGTTGACCTTCCAACAGCATGGGGGCGGTGACCTCCACCCA 

ATAGAAAATCCTCTTATAACTTTTGACTCCCCAAAA

(1-1459) Sequence 17, Application US/08904809

Significance = Mismatches = Optimized Score = 240 Matches = 262 Conservative Substitutions Optimized Score Matches 56 34% 15 Initial Score Residue Identity =

AGGCCGACCAAGAGCCAGGGGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCAGAGTACAAGAAC 100

CAACCICAGGGGTGCTGGTANTGCCTGCC--ATCAANAAGGTTATGGGTTCCCAGGAAAATTCACTC
AACCATTCCTGACGTTGCTGGTANTGCCTGCC--ATCAANAAAGATTATGGGTTCCCAGGAAAAATTCACTC
510 520 530

27. US-09-030-606-174 (1-1459) US-09-020-747-17 Sequence 17, Application US/09020747 Initial Score = 56 Optimized Score = 240 Significance = 0.30 Residue Identity = 34% Matches = 262 Mismatches = 478 Gaps = 15 Conservative Substitutions = 0

  28. US-09-030-606-174 (1-1459) US-09-020-747-11 Sequence 111, Application US/09020747 Initial Score = 56 Optimized Score = 420 Significance = 0.30 Residue Identity = 37% Matches = 514 Mismatches = 763 Gaps = 107 Conservative Substitutions = 0

US/08904809

```
1330 1340 1350 1360 1370 1380 1390 GRAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGTTGAATTGCTTGAATATGGGAGGCAGAGGTTGAAGTGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGAGAAAGGCATTTTATAGCCT-----GGGCATAAGTGAAATCAGCAGAGCCTCTGGGTGGATGTGTA
1200 1210 1220 1230
                                                                                                                                                                                                                                                                                                                                                                                                                       LU4U 1050 1060 1070 1080 1090 1100 GTATAAGTGGACTTGTGCAAGGGTTGTTCAAGGGTCAACTGTGTACCCAGAGGGAAACAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                        GGCACCCTGGCAAGCAGTGATTGGGGGAGGGGATCTAACAATGTCACTTGGGCCAGAATGGACC
900 910 920 930 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ACCACTCTTTAGCGATGCCT
1010 1020
                                                                                                                                                                                                                                                                                             10 830 840 850 860 870 880 TCCCCAAAAACCTGACTAGAAAT----AGCCTACTGTTGACGGGAGCCTTACCAATAACATAAATAGTCG
                                                                                                                                                                                                                                                  ATTIATGCATACGTTTTATGCATTCATGATATACCTTTGTTGGAATTTTTTGATATTTCTAAGCTACAGT
                                                                                                                                                                                                                                                                    ---AGGCTCAAGTGCTGTGGCTTCACCAACTATACGGATTTTGAGGACTCACCTTCAAAGAGAACAG
560 570 580 590 600
610 620 630 640 650 660 670
GAGAGACACACAGGGAGACAGTGAGAGAGAGAACTGAGAGAAACAGAGAAATAAACACAGGAATA
                            TGCCCTTTCTGCTCCAGACTTGGGGCTAGATAGGG-----0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGGCACTTCAAA
1240
                                                                                                                                                                                                                                                006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1260
                                                                                                                                                                                                                                                 890
                                               490
```

```
AAGGGATGAAAAAGGACACATGCTTCCTTTGAGGAGACTTCATCTCACTGGCCAACACTCAGTCACT
520 530 540 550 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1380 1400 1410 1420 1430 1440
GCAGAGGTTGAAGTTGAGATCACCACTATACTCCAGCTGGGGCAACAGAGTAAGACTCTGTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                 1020 1030 1040 1050 1060 1070 1080
GITTATIGAAAAAATCCAAGIATAAGIGGACTIGTGCAITCAAACCAGGGTTGTTCAAGGGTCAACIGTGTA
                                                                                                                                                                                           GATCAAGGCAGGAAAATGANTATAACTAATTGACAATGGAAAATCAATTTTAATGTGAATTGCACATTATCC
170 180 190 200 200 210 220
                                                                                                                950 960 970 980 990 1000 1010 TITCIAAAGTIGTIGCAACTCTCCIAAAAITTTTTTGAIG--T
                                                             Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30. US-09-030-606-174 (1-1459)
US-09-020-747-46 Sequence 46, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
                            Optimized Score = 201
Matches = 227
Conservative Substitutions
US-09-030-606-174 (1-1459)
US-08-904-809-46 Sequence 46, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score
                             378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAAAAAAAAA
                            Initial Score = Residue Identity = Gaps =
```

```
AATAACATAAATAGTCGATTTATGCATTTATGCATTCATGATATACCTTTGTTGGAATTTTTTGATA
                                                                                                      ACTTTTTATTTAAATGTTTATA
X
                                                                                                                                                                                                                                                          1380 1390 1400 1410 1420 1430 1440 GCAGAGGTTGAAGTTGAGATCACCACTATACTCCAGCTGGGGCAACAGAGTAAGACTCTGTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00 1310 1320 1330 1340 1350 1350 1370 GATATGGTGGCGCGCGTGTGCTTGGGTGGCTGAGGCAGGAGAATTGCTTGAATATGGGAG
                             820 830 840 850 TTTGACTCCCCAAAAACCTGACTAGCCTAACC
                                                                                                                                                                                                                                                                                     TTTAAAAGCTTTCAAAANAANAATTATTGCAGTCTANTTAATTCAAACAGTGTTAAATGGTATCAGGATAA
240 250 250 260 270 280 290
   Mismatches
= 227
Substitutions
Matches
Conservative
                                                                                    900
                           800 810 AAATCCTCTTATAACT
Residue Identity
Gaps
```

540

530

550

10 GGTCAGCCGCACACTG

472

Optimized Score = 236 Significance Matches = 257 Mismatches Conservative Substitutions

(1-1459) Sequence 13, Application US/08806596

31. US-09-030-606-17 US-08-806-596-13

Initial Score Residue Identity Gaps

X 1450 AAAAAAAAAAAAAAA

GT 590 Sequence 13, Application US/09020747

580 590 600 610 620 630 640 AGGGCCGCATGCAGAGAGAGACACACAGGAGACAGGAGACAGAGAGAACTGAG 440 450 460 470 480 490 500 TAAGCICTATGTGTTCTGCGCGGGGGGGGAGGCCAGGAAGAAGGACTCCTG GACGTTGCTGGTAATGCCTGCCATCAANAAAGATTATGGGTTCCCAGGAANACTTCACTCAAGTGTTGGAA 480 490 500 500 510 510 | 340 | 350 | 350 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 310 | 320 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 | 330 370 380 390 400 410 420 430 CTGCGTCCCAGGCAGAATGCCTACCGTGCTGCAGGCGTGCTGGTGTCTGANGAGGTCTGCAN 80 90 100 110 120 130 140 AGGCCGACCAAGAGCCAGAGGCCAGCCTCTCCGTACGGCACCCAGAGTACAACAGAC AGCTGTTTGTCCTTTGTGGANCCTCAGCAGTNCCCTCTTTCAGAACTCANTGCCAAGANCCCTGAACAGGA 50 50 100 110 150 160 170 180 190 200 210 CCTTGCTCGCTAACGACCTCATCCGGAGCAATCCGTGTCCGAGTCTGACACCATCCGGAGCA GCCACCATGCAGTGCTTCAGTTAAGACCATGATGATCTCTTTCAATTTGCTCATCTTTCTGTGTGT 120 130 140 150 150 20 30 40 70 70 TTTCCAGAAGTGAGTGCACAGTCCTACACATCGGGCTGGGCCTGCACAGTCTTG GAGCCAGGCGTCCTTGCTGCCACTCAGTGGCAACACCCGGCX 10 20 40 Conservative Substitutions 10 GGTCAGCCGCACACTG 410 Gaps

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590 620 630 640 AGGCCGCATGGAGAGAGACACACAGGGAGACAGTGACAACTAGAGAAAACTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 450 460 470 480 490 500
TAAGCTCTATGACCCGCTGTACCACCCCANCATGTTCTGCGCCGGGGGGGGAGGCCAAGACCAGAAGGACTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGTÍGCTGGTAATGCCTGCCATCAANAAAGATTATGGGTTCCCAGGÁANACTTCACTCAAGTGTTGGÁA
480 530 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCACCATGAAAGGGCTCAAGTGCTGTGGGTTCNNCCAACTATAGGG----ATTTTGAAGANTCACCTACT
550 560 570 580 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTCATCTTCATTGCTGAGGTTGCTGTGGTCGCCTTGGTGCTGACCCACAATGGCTG-AGCACTTCCT 410 420 440 450 450 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEGAGCICACGGGTGTGTGTCTCTTCAAGGAGGTCCTCTGCCCAGTCGCGGGGGGTGACCCAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGITÍCCTGGGCTGCTATGGTGCTGAGAGCAAGTGTGCCCTCGTGACGITCTTCTTCATCCTCCT 340 380 390 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GICGICCAGGCCATGCAGTTGTCAACGTGGGCTACTTCCTCATCGCAGCGGCGTTGTGGTCTTAGCTCT

270 280 290 300 310
                                                                                                                                                                                                                                                  AGCTGTTTGTCCTTTGTGGANCCTCAGCAGTNCCCTCTTTCAGAACTCANTGCCAAGANCCCTGAACAGGA 50 50 100 100 110
                                                                                                                                                                                                                                                                                                              150 160 170 180 190 200 210 CETTGCTCGTTCGCTCTCATCCGGAGCA
                                                                                                                                                                                                                                                                                                                                                                      220 230 240 250 260 270 280 TCAGGGGGGAACTCTTGCCTCGTTTCTGGCTGGGGTCTGCTGGCGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGCCCTG-TTGGCAGTGGGCATCTGGGTGGGGCATCCTTTCTGAAGATCTTCGGGCCACT
GCAGCCCTG-TTGGCAGTGGGCATCTGGGTGTCAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACT
SCAGCCCTG-TTGGCAGTGGGCATCTGGGGCATCCTTTCTGAAGATCTTCGGGCCACT
                                                                                                                GAGCCAGGCGTCCCTCTGCCTCAGTGGCAACACCCGGG X 10 20 30 40
                                                                                                                                                                                               10 20 20 30 30 40 50 50 50 50 60TCCACACACTACACCATCGGCCTGGGCCTGCACACTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAAGAAAANAGTGCCTTTCCCCCATTTCTGTTGAATTGACAAACGTCCCCAACAGAATTG----
620 630 640 680
                  472
Optimized Score = 236
Matches = 257
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -AAACCTGCACCCAACCCAANGGGTCCCCAACCANAATTNAAGGG 710 710 720 X
         II II A
      Initial Score
Residue Identity
Gaps
```

800 ATAGAAAATCCTCTT

## ATAGAAAATCCTCTTA

'4 (1-1459) Sequence 7, Application US/09071710 34. US-09-030-606-17 US-09-071-710-7

Significance Mismatches Optimized Score = 81 Matches = 103 Conservative Substitutions Initial Score
Residue Identity -

590 610 CACACAGGGCCGCATGGCAGAGAGACACAG

'4 (1-1459) Sequence 7, Application US/09525397 35. US-09-030-606-17 US-09-525-397-7

 $0.27 \\
120$ Significance Mismatches Optimized Score = 81
Matches = 103
Conservative Substitutions 54 44% 10 Initial Score Residue Identity Gaps

590 610 cacacagegecegeagagatecagagacacag

US/08850713 US-09-030-606-174 (1-1459) US-08-850-713-8 Sequence 8, Application 36.

0.27 120 0 Significance Mismatches Optimized Score = 81
Matches = 103
Conservative Substitutions 54 448 10 9 H H Initial Score Residue Identity Gaps

1 (1-1459) Sequence 7, Application US/09841894A 37, US-09-030-606-174 US-09-841-894A-7

0.27 120 0 Significance Mismatches Optimized Score = 81
Matches = 103
Conservative Substitutions Optimized Matches 54 448 10 0 0 0 Initial Score Residue Identity Gaps

GCCAGTTTCTGTTGCTGCCAAA X 10 20

US-09-030-606-174 (1-1459) US-09-020-747-98 Sequence 98, Application US/09020747 38.

80

70

9

30 140 TACAACA(         GGCTATA	ATCCGGA       CACCAAG   18   280   CTGGCGA           CGAGGAA	ACCCAGA   AAGGTCC 32 43 AGGTCTG     CCATGGG 290	AGGACTC	Initial SCG Residue Ide Gaps TGCATA	TGTGAAT 	1110 1110 1110 1110 1110 1110 1110
Initial Score = 54 Optimized Score = 161 Significance = 0.27  Residue Identity = 38% Matches = 185 Mismatches = 276  Gaps = 19 Conservative Substitutions = 0  400 410 420 430 440 X 450 460  AGTGCGTGAACGTGTGTGTGTGTGTGTGTACCACCCCANCA  AGTGCGTGAACGTGTGTGTGTGTGTGTGTGTACCACACAAAA  X 10 20	470 480 490 500 510 520 530  TGTTCTGCGCGGAGGGCAAGACCACTGCAACGTGAGAGGGGAAAGGGGAGGCAGGC	100	TTCCAACAGCATGGGCCTGAGGGCGTGACCTCCAATAGAAAATCCTCTTATAACTTTTGACTCCC	900 910 920 x 930 940 950  ACGITTATGATATACCITTGITGGAATTITITGATATTICTAAGCTACACAGTICGICTGIGA  1	39. US-09-030-606-174 (1-1459) US-09-020-747-94 Sequence 94, Application US/09020747  Initial Score = 54 Optimized Score = 162 Significance = 0.27  Residue Identity = 36% Matches = 180 Mismatches = 305  Gaps = 14 Conservative Substitutions	10 20 30 40 x 50 60 70  GGTCAGCCGCACACTTTCCAGAAGTGAGGTGCAGAGCTCCTACACCATCGGCTGGGCTGCACAGTCTTG

```
40 1050 1060 1070 1080 1090 1100
GGACTIGIGCATTCAAACGGTCAAGGGTCAACTGTGTACCCAGAGGGAAACAGTGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCCCTCCTCCTCAGGCTATGAGG---ACAGCTATCATAAGTCGGCCCAGGCATCCAGATACTAC
0 110 120 130 140 150 160
                                                                                                                                                                                                                                                                                                                                              ACGTAGACCATCCAACTTGTA
X 10 20
                                                                                                                                                                    150 160 170 180 190 200
AGACCCTIGCTCACCACCATCAAGTIGGACGAATCCGIGTCCGAGTCTGACACC
                        Optimized Score = 104 Significance = Matches = 125 Mismatches = Conservative Substitutions =
                                                                                                                                                                                               440
                                                                                                                                                                                                                                                                               030-606-174 (1-1459)
020-747-14 Sequence 145, Application US/09020747
                                                                                                                                                                                                                                 52
40%
10
50
                                                                                                                                                                                                                                                            ACACAGGGCCG
                                                                                                                                                                                                                                                                                                   core =
dentity =
40
```

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41. US-09-030-606-174 (1-1459) US-08-806-596-7 Sequence 7, Application US/08806596 Initial Score = 52 Optimized Score = 248 Significance = 0.29
Residue Identity = 33% Matches = 284 Mismatches = 53
Gaps = 28 Conservative Substitutions = (

 90 100 110 120 130 140 150 160 GGGACCCAGAGTACAACAGACCCTTGCTCGCTAACGAC GGGACCCTTGCTCGCTAACGAC GCTAACGAC GCTAACGAC GCTAACGAC GCTAACGAC GCTAACGAC GCTAACGAC GCTAACGAC GCTAACGAC GCTAACGAC GCTAACAACAATTAAAAATACGAGCCCTATTTCAAAGATTTTAAGGGAATTAAA 30 40 50 60 70 70 80 90

 960 ACAGTTCGT 12. US-09-030-606-174 (1-1459) US-09-020-747-13 Sequence 132, Application US/09020747 Initial Score = 49 Optimized Score = 111 Significance = 0.21
Residue Identity = 37% Matches = 122 Mismatches = 200
Gaps - 7 Conservative Substitutions = 0

 | 520 | 530 | 540 | 550 | 560 | 570 | 580 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590

 | 810 | 820 | X | 830 | 840 | 850 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 |

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43. US-09-030-606-174 (1-1459) US-09-020-747-86 Sequence 86, Application US/09020747  Initial Score = 48 Optimized Score = 155 Significance = 0.19 Residue Identity = 35% Matches = 294 Residue Identity = 18 Conservative Substitutions = 0.19 Gaps = 18 Conservative Substitutions = 0.19  #10	480 490 500 510 520 530 540  GCGGAGGCAAGGACTCCTGCAACGTGAGAGGGGAAGGGGAGGCAGCCACTCAGGAAG  GCGGAGGCCAAGGACTCCTGCAACGTGAGAAGGGCAGGCA	620 630 640 650 660 670 680  GGAGACAGTGACAACTGAGAAACTGAGAAACAGGAATAAAGAGAAAGGAAAGGAAAGGAAAGGAAAGGGAAGGAAAGGGAAAGGGAAAGGGAAAGGGAAAA	770 780 790 800  GGGGCCTGAGGGCGGTGACCTCCACCCAATAGAAAATCC  CATGGGACAGAGCCATTGATTTAAAAAGCAAATTGCAT  310 320 860 870  AGAATAGCCTACTGTTGACGGGGAGCCTTACCAATAAC  AGAAATAGCCTACTGTTGACGGGGAGCCTTACCAATAAC  AGAAATAGCCTACTGTTGACGGGAGCCTTACCAATAAC  AGAAATAGCCTTCTACTACTTCACCAGACACTCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACTCCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACTCCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACCTCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACTCCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACTCCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACTCCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACTCCTTTTC  AAGAATAGCCTTTCTACTTCACCAGACACTCCTTTTC  AAGAATAGCCTTTCTACTTCTACTTTTTTTTTT	910 920 x 940 950 960 970 TGCATTCATGATATTTTTTTTTTTTTTTTTTTTTTTTTT	### ### ##############################	10 20 30 40 50 60 70 CGCACACTGTTCCAGAAGTGAGCTCCTACACCATCGGGCTGGGCTTGAAGTTTTGAAAGAAGGGATGGTG

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00 810 820 830 840 850 860 870
ATCCTCTTATAACTTTTGACTCCCCAAAAACCTGACTAGAAATAGCCTACTGTTGACGGGGAGCCTTACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   730 740 750 760 770 780 790
CACACACATAGAAATGCAGTTGACCTTCCAACAGGGGGGGCGGTGACCTCCAGCAATAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 530 540 550 560 570 580
AGAGAGGGGAAAGGCGACTCAGGGAAGGGTGGAGAAGGGGGAGACAGAGACACAGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 380 390 400 410 420 430
CCAGGCAGAATGCCTACCGTGCTGCGTGTCGGTGTCTGANGAGGTCTGCANTAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGTCGTATTACGCGCGCTCACTGGCC----GTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGGC-
440 440 450 460 500 460 500
                                                                                                                                                                                                                                                          230 240 290 290 270 280 290 290 TGCTTCGCAGCGAGCGGTGAGCTTCTCGCTGCGGGGTGACCGTGAGCTTAGCTTCTTCTGCTTGGCTGGGGTTGGTGAGCTTGTTGGTGAGTTTGCAATTGCAAATACATCTGCAAATTCTTGGCAATTGGCAATTGCAAATACATCTGAAATTGGCAATTGGCAATTGGCAATTGTGGCCAAT 170 180 200 210 220 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 310 320 330 340 350 360 cacegerence cacegorian 
                                                                                                                                                                                            160 170 180 190 200 210 220 cGCTAACGACCTCATGCTCATGCTCATGCTCAGCATCAGCATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCAT
                                                        CCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCTCCGTACGGCACCCAGAGTACAACAGACCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880 890 900 910
TAACATAAATAGTCGATTTATGCATTC
```

0.19

250 Significance

Optimized Score

48

US-09-030-606-174 (1-1459) US-08-904-809-3 Sequence 3, Application US/08904809

					•		• • •		,			<b>v</b> .
Residue Identity = 35% Matches = 282 Mismatches = 491 Gaps = 31 Conservative Substitutions = 0	10 20 30 40 50 60 70 CGCACACTGTTTCCAGAAGTGCAGAGCTCCTACACCATCGGGCTGGGCCTGCACAGTTTGAGGCCGA CGCACACTGTTTCCAGAAGGGCTGAGCCGA CTTTTGAAAGAAGGATGGCTG X 10 20	80         90         100         120         130         140         150           CCAAGAGCCAGGCCAGCCTCTCCGTACGAGTACAACAGACCTTGCT           I   I   I   I   I   I   I   I   I   I	160	230 240 250 260 270 280 290  TGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCCTCGTTTCTGGCTGG	300 310 320 330 340 350 360 CACGGGGGGTGTCTGCCCTTCAGGGGGGGGTGTGTCCCAGAGCTCTGCGTC.	370 380 390 400 410 420 430 CCAGGCAGAATGCCTACCGTGCTGCAGTGCTGTGTCGGTGTCTGANGAGGTCTGCANTAAGCTC	440         450         460         470         480         490         500         510           TATGACCCGCTGTACCACCACCACCACCACCTGCCAACGTG           I	520 530 540 550 560 570 580  AGAGAGGGAAAGGGAGGCAGCCACTCAGGGAAGGGTGGAGAAGGGGAGACAGAGACACAGAGCCG	590 600 610 620 630 640 650 .  CATGGCGAGATGCAGAGACACACACAGGAGACACTGACAACTAGAGAGAAACTGAGAGAAACA  CATGGCGAGATGCAGAGACACACACACACAGAGAGAACAACTAGAGAGAAACA	660         670         680         690         710         720           GAGAAATAAACAGGAATAAAGAAAGGAAAGGAAAGGAAA	730 740 750 760 770 780 790  CACACACATAGAAATGCAGTTGACCTTCCAACAGGGGGGCGTGACCTCCACCCAATAGAAA  [	800 810 820 830 840 850 860 870 ATCCTCTTATAACTTTGACTCCCCAAAAACCTGACTAGAAATAGCCTACTGTTGACGGGGAGCCTTACCAA

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10 20 30 40 50 60 70 CGCACACTGTTTCCAGAAGTGAGTGCAGAGCTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGA
                                                                                                                                                           CTTTTGAAGAAGGGATGGCTG
                                                                                                                                                                                                                80 90 100 110 120 130 140 150 CCAAGAGCCAGGCAGCCAGAGCCCAGAGCCCTTGCT
                                                                                                                                                                                                                                                       160 170 180 190 200 210 220 CGCTAACGACCTCATGCAAGTTGGACGAATCCGTGTCCGAGTCTGACCATCCGGAGCATCAGCAT
                                                                                                                                                                                                                                                                                                                                                                              370 380 390 400 410 420 430 CCAGGCAGAATGCTACCGTGCTGCAGTGTCTGAACGTCTGAACGTCTGAAGGTCTGCAATAAGCTC
                                                                                        0.19
                                                                                       250 Significance - 282 Mismatches -
                                                                                                                                                                                                                                                                                                                                                                             350
                                                         US-09-030-606-174 (1-1459)
US-09-020-747-3 Sequence 3, Application US/09020747
                                                                                        Optimized Score - 250
Matches - 282
Conservative Substitutions
760
                   880 890 910
TAACATAAATAGTCGATTTATGCATTC
                                                                                         48
358
31
730
                                                                                      Initial Score = Residue Identity = Gaps =
720
                                                           46.
```

```
00 810 820 830 840 850 860 870 ATCTCTTATAACTTTGACGGGGGGCCTTACCAA
                            TTCNCCTTTCTTCCTTTCTTCNCNCTTTCCCCCGGGGTTTCCCCCNTCAAACCCCNA
720 730 740 750 750
                                                                      800
```

# 880 890 900 910 TAACATAAATAGTCGATTTATGCATTC

(1-1459) Sequence 51, Application US/08904809 47. US-09-030-606-174 US-08-904-809-51 S  $0.18 \\ 105 \\ 0$ Significance Mismatches Optimized Score = 82
Matches = 99
Conservative Substitutions 82 99 47 468 11 Initial Score Residue Identity =

GTCCTAGGAAGTCTAGGGGACA 

### 860 870 880 GACGGGGAGCCTTACCAATAACATAAA

48. US-09-030-606-174 (1-1459) US-09-020-747-51 Sequence 51, Application US/09020747

 $\begin{array}{c} 0.18 \\ 105 \\ 0 \end{array}$ Significance = Mismatches = = = Optimized Score = 82
Matches = 99
Conservative Substitutions 47 468 11 Initial Score = Residue Identity =

GTCCTAGGAAGTCTAGGGGACA 710

US-09-030-606-174 (1-1459) US-09-020-747-11 Sequence 115, Application US/09020747

 $0.18 \\
209$ Significance = Mismatches = = Optimized Score = 132 Matches = 153 Conservative Substitutions 47 418 10 9 0 0 Initial Score Residue Identity = Gaps

US-09-030-606-174 (1-1459) US-09-020-747-13 Sequence 139, Application US/09020747

Optimized Score = 124 Matches = 138 Conservative Substitutions 47 348 16 Initial Score Residue Identity Gaps

us-09-030-606-174.res

  51. US-09-030-606-174 (1-1459) US-08-904-809-72 Sequence 72, Application US/08904809 Initial Score = 47 Optimized Score = 170 Significance = 0.18
Residue Identity = 37% Matches = 191 Mismatches = 310
Gaps = 10 Conservative Substitutions = 0

 | 540 | 550 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600

| 750 | 760 | 770 | 780 | 790 | 800 | 810 | 810 | 810 | 800 | 810 | 800 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810

890 900 TCGATTTTATGCATTCATGATAT

52. US-09-030-606-174 (1-1459) US-08-806-596-4 Sequence 4, Application US/08806596 Initial Score = 47 Optimized Score = 264 Significance = 0.18
Residue Identity = 34% Matches = 292 Mismatches = 533
Gaps = 19 Conservative Substitutions = 0

 ATTCCGGTTTCCCCNAATCCGGGGANANCC

CATGCCTG

74 (1-1459) Sequence 4, Application US/08904809 53. US-09-030-606-1 US-08-904-809-4

.0.18 292 Mismatches Optimized Score = 264
Matches = 292
Conservative Substitutions Initial Score = Residue Identity = Gaps = =

390

CATGCCTG

54. US-09-030-606-174 (1-1459) US-09-020-747-4 Sequence 4, Application US/09020747

0.18 466 0 220 Significance 264 Mismatches Optimized Score = 220
Matches = 264
Conservative Substitutions 47 348 25 Luitial Score Residue Identity = Gaps

ccrccrddgrccracrdaccrd

us-09-030-606-174

   

#### AAAAAAAAAAAA

55. US-09-030-606-174 (1-1459) US-09-020-747-19 Sequence 19, Application US/09020747 Initial Score = 46 Optimized Score = 216 Significance = 0.16
Residue Identity = 32% Matches = 238 Mismatches = 486
Gaps = 11 Conservative Substitutions = 0

  GAATTTTTGATATTCTAAGCTACACAGTTCGTCTGTGAATT

56. US-09-030-606-174 (1-1459) US-08-904-809-59 Sequence 59, Application US/08904809 Initial Score = 45 Optimized Score = 118 Significance = 0.15
Residue Identity = 38% Matches = 129 Mismatches = 201
Gaps = 8 Conservative Substitutions = 0

Thu May

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ATGACAAGTTATCAAAAACTCACTCACTTTTTCACCTGTG---CTAGCTTGCTAAAATGGGAGTTAACTCTAG 130 140 150 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1190 1200 · 1210 1220 1230 1240 1250
AATCCCAGCACTTTGGGAGGCAGGCAGGCAGTCACTTGAGGTAAGGAGTTCAAGACCAGCCTGGCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 980 990 1000 1010 1020 1030 1040 TITITIAAAITGITGCAACTCTCCTAAAAITTITCTGAIGTGTTITATIGAAAAAAICCAAGTATAAGIGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTTATCA----GCAAAACTGGTGATGGCTACTGAAAAGATCCATTGAAAATTATCATTAATGATTTAAA
30 40 50 50 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1050 1060 1070 1080 1090 1100 1110 TGTGCATTCAAACCAGGGTTGTTCAAGGGTCAACTGTGTACCCAGAGGGAAACAGTGACACAGATTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 910 920 930 940 950 970 970 970 950 970 970 970 970 970 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAACAATGGGTTGTGAGGAA X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1310 1270 1230 x 1300 1310 1320 1330 136GTGGTGAAATCCTGTCTGTAAAAATACAAAAGTTAGCTGGATATGGTGGCAGGCGCCTGTAATCCCAGCT
                                                                                                                                                                                  1190 1200 1210 1220 1230 1240 1250
AATCCCAGCACTTTGGGAGGCGAGGCAGATCACTTGAGGTAAGGAGTTCAAGACCAGCCTGGCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                            980 990 1000 1010 1020 1030 1040 TITITIAAATIGIACAACICCTAAAATTTTTCTGAIGIGITTAITGAAAAAATCCAAGTATAAGTGGAC
900 910 920 930 940 950 960 970 GILITANGCATTCANGATATTTCTAAGCTACACAGTTCGTCTGTGAAT
                                          ACAACAAATGGGTTGTGAGGAA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118. Significance = .
129 Mismatches = .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-1459)
Sequence 59, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTTTGAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45
388
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57. US-09-030-606-1
US-09-020-747-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGTCTTTATTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial Score Residue Identity Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTGG
```

```
910 920 930 940 950 960 970 TITATGCATTCATGA-TATACTTTTTGATATTTCTAAGCTACACGTTCGTCTGTGAATT
                                                                                                                                                                                                                                                                                                                                                                                             840 850 860 870 880 890 900
GACT----AGAAATAGCCTACTGTTGACGGGGAGCCTTACCAATAACATAAATAGTCGATTATGCATACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTITATCTACTGGCTATGAAA
                                                                                                                                                                                                                                                                                                      0.15
486
0
                                             60 1270 1280 X 1300 1310 1320 1330
TGGTGAAATCCTGTCTGTACTAAAAATACAAAGTTAGCTGGATATGGTGGCAGGCGCCTGTAATCCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 Significance
238 Mismatches
                                                                                                                                                                                          Optimized Score = 148 Significance
Matches = 174 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59. US-09-030-606-174 (1-1459)
US-08-904-809-19 Sequence 19, Application US/08904809
                                                                                                                                                              58. US-09-030-606-174 (1-1459)
US-09-020-747-12 Sequence 125, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCTAGCCCTCTGTCAGAGCAAACCTCAGTGCCTCTCTTTGCTTGT
TTTCTAGCCCTCTGTGAGAGCAAACCTCAGTGCCTCTTTGCTTGT
430 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score = 216
Matches = 238
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1050 1060 1070
TGTGCATTCAAACCAGGGTTGTTCAAGG
                                                                             TCGTCTTTATTGGACTTCTTTGAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
32%
11
                                                                                                                                                                                             45
408
10
                                                                                                                                                                                                  H ( H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score
Residue Identity
Gaps
                                                                                                                                                                                                  Initial Score
Residue Identity
```

 60. US-09-030-606-174 (1-1459) US-09-020-747-26 Sequence 26, Application US/09020747

Initial Score = 45 Optimized Score = 233 Significance = 0.15
Residue Identity = 30% Matches = 247 Mismatches = 570
Gaps = 5 Conservative Substitutions = 0

 | 310 | 320 | 330 | 340 | 350 | 360 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 380 | 370 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380

 | 40 | 750 | 760 | 770 | 780 | 790 | 800 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 820 | 830 | 840 | 850 | 860 | 860 | 810 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 | 820 |

```
CITITICNCTACCNCCNNTTCTTTGCCTCTCTTNGATCATCCAACCNTCGNTGGCCNTNCCCCCCCNNNTC 750 760 770 770 780 790 800
                                                                                   960 X 970 980 990 1000 1010 CAGITCGICTGTGAATITITITAAATIGTIGCAACTCTCCTAAAATITITICTGATGTG
                                                                                                                                                                       CTTTNCCC
820
```

Sequence 48, Application US/08904809 61. US-09-030-606-17. US-08-904-809-48 0.14 Significance Mismatches Optimized Score = 50
Matches = 50
Conservative Substitutions 44 408 0 Initial Score = Residue Identity = Gaps

1050 

1130 CACGAAGA

62. US-09-030-606-174 (1-1459) US-09-020-747-48 Sequence 48, Application US/09020747

50 Significance 50 Mismatches Conservative Substitutions Optimized Score Matches 44 408 0 Initial Score Residue Identity =

AGGCATTTTTCTCTTATATACATAAATGATATTTTTGCAANTATANAAATGTGTCATAAATTATAAATG 

1130 CACGAAGA

63. US-09-030-606-174 (1-1459) US-08-904-809-67 Sequence 67, Application US/08904809

0.14 Significance = 127 Optimized Score 44 Initial Score

```
1000 1010 1020 1030 1040 1050 1060 CTCCTAAAATTTTTTTTGATTTTATTGAAAAATCCAAGTATAAGTGGACTTGTGCATTCAAACCAGGGT
                                                                                                                                                                       20 930 940 950 960 970 980 990
ACCITIGITGGAAITITITGATATTCTAAGCTACACAGTICGICTGTAAAITTTTTTAAATTGTTGCAACT
                                                                                                                             850 860 870 880 890 900 100 TACTETTGACGGGGGGGGGCCTTACCAATAAATAGTCGATTTATGCATTTATGCATTTATGCATTCATGATAT
                                 ACTACACACACTCCACTTGCCC
                                                                                                    720 770
TGGGGAGGCA--GAAACACACACATAGAAATGCAGTTGACCTTCCAACAGCATGGGGCCTGAGGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1070 X 1080 1090 1100 1110 1120 TGTTCAAGGGTCAACTGTGTACCCAGAGGGAAACAGTGACACAGATTCATAGAGGTGAAA
Matches = 150 Mismatches
Conservative Substitutions
     38%
16
        11
       Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGGACCGT
380 X
```

ACTACACACACTCCACTTGCCC  $0.14 \\ 226$ 127 Significance = 150 Mismatches = Optimized Score = 127
Matches = 150
Conservative Substitutions 44 38**%** 16 Initial Score = Residue Identity = East

64. US-09-030-606-174 (1-1459) US-09-020-747-67 Sequence 67, Application US/09020747

GAGACCTGATCT 230	990 TGTTGCAACT         GCTTGCCT	1060 ACCAGGGT 	
	980 TTTTAAATTG         CTTAGTCTGC	1050 GTGCATTCAA      TACCATAGTT	1120 GTGAAA
AGTTCTCCTC7	970 CTGTGAATTTTTTA                    CTCAGCACTCCTTAG 280 290	1040 AAGTGGACTT 	1110 ATTCATAGAG
	20         930         940         950         960         970         980         990           ACCTITGITGAATTITITAATTICTAAGCTACACACTICGICGAATTITITAAATTIGITGCAACT         1   1   1   1   1   1   1   1   1   1	1000 1010 1020 1030 1040 1050 1060  CTCCTAAAATTTTCTGATGTTTATTGAAAAATCCAAGTATAAGTGGACTTGTGCATTCAAACCAGGGT	TGTTCAAGGGTCAACTGTGTACCCAGAGGAAACAGTGACACAGATTCATAGAGGTGAAAAAACAGTGACACAGATTCATAGAGGTGAAAAAAAA
   GGAGATTCAC   200	950 TTCTAAGCTAG 	TATTGAAAAA TATTGAAAAAA 	1090 AGAGGGAAAC
l l rerecrerect 190	940 TTTTTGATAT'   111 GTCTTGCACA'	TO10 CTGATGTGTT GCCTGGCCAC	CTGTGTACCC
	930 TTGTTGGAAT7   111 AGGCTGGGCAC	1000 TAAAATTTTTC     CAGGGCCCCA( 310	TGTTCAAGGGTCAAG TGTTCAAGGGTCAAG 
TTGTG 170	920 ACCTT TTAGA	CTCCT  - -  CTCCC	TGTTCP TGTTCP       AGTGGP

65. US-09-030-606-174 (1-1459) US-09-020-747-16 Sequence 164, Application US/09020747 Initial Score = 44 Optimized Score = 148 Significance = 0.14
Residue Identity = 36% Matches = 174 Mismatches = 288
Gaps = 11 Conservative Substitutions = 0

510

ACTCCTGCAACGTGAGAGAG

66. US-09-030-606-174 (1-1459) US-08-904-809-32 Sequence 32, Application US/08904809 Initial Score = 44 Optimized Score = 225 Significance = 0.14
Residue Identity = 32% Matches = 258 Mismatches = 519
Gaps = 20 Conservative Substitutions = 0.0

 US-08-904-809-74 Sequence 74, Application US/08904809

```
310 1320 1330 1340 1350 1360
GCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGAGGAGAATTGCTTGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 1020 1030 1040 1050 1060 1070 1080 GTGTTTATTGAAAAAAAAATCCAAGTGTATAATGTGGACTTGTGCATTCAAACCAGGGTTGTTCAAGGGTCAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTANATICTICCIGAAGGCCAGCGCIIGIGGAGCIGGCANGGGICANIGITGIGIGIAACGAACCAGIGCI
310 320 330 330 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              940 950 960 970 980 990 1000
GATATTICTAAGCTACACAGTICGICGAATTITITAAAITGITGCAACTCICCTAAAATTITICIGAT
                                                                                                                                                                                                                                                                        ACTTCCAGGTAACGTTGTT X
                                                                                                                                                                                                                                                     800 810 820 830 840 X 850 860
TAGAAAATCCTCTTATAACTTTTGACTCCCCAAAAACCTGACTAGAAATAGCCTACTGTTGACGGGGGGGCCT
                                     NGGCAAGNTGGCTTCGGGCCCCCGGTGGGCCCNNCTCTAANGAAAACNCCNTC--CTNNNCACCAT
670 680 690 730
                                                                                                                                                                                                Optimized Score = 162 Significance
Matches = 180 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCCCNNGNNACGNCTANCAANGNATCCCTTTTTTANAAACGGGCCCCCCNCG 740 750 760 760 770 780 X
                                                                                                                                                                  67. US-09-030-606-174 (1-1459)
US-09-020-747-15 Sequence 159, Application US/09020747
                                                                                                                     1080 1090 1100
GTCAACTGTGTACCCAGAGGGAAACAGTGACAC
                                                                                                                                                                                                       Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1010
                                             1000
```

68. US-09-030-606-174 (1-1459)

```
1070 1080 1090 1100 1110 1120 1130
TCAAGGGTCAACTGTGTACCAGAGGGAAACAGTGACACAGATTCATAGAGGTGAAACACGAAGAAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1000 1010 1020 1030 1040 1050 1050 CTAAAATTTTTTTTTGAATGTTATTGAAAAATCCAAGTATAAGTGGACTTGTGCATTCAAACCAGGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                          850 860 870 880 890 900 910 920 TGTTGACGGGGGGGGGCCTTACCATAACATAAGTCGATTTATGCATATATGCTTTTATGCATTTATGCATTATGCTTATGCATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                930 940 950 960 970 980 990
TTTGTTGGAATTTTTTGATATTTTCTAAGCTACACAGTTCGTCTGTGAATTTTTTAAATTGTTGCAACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATT----AGGCTTTTGATTTATAANACTTTGGGTACTTATACTAAATTATGGTAGTTATACTTCAG
310 310 320 330 340 350 360
                                                                                                                                                                                                                                                                                                   TACCACTCTAATCAGAAATTACAGACTCTGATTCTACAGTGATGATTGAATTCTAAAATGGTAATC
230 240 250 260 250
                                                                                                                                                710 720 730 740 750 750 770 cagacagaaggcagaaaaacacacatagaaaatgcagtigaccttccaacagcatggggcctgaggg
                                                                                                                          TTTCATAGGAGAACACACTGAG
                                                                                                                                                                                                                          190 Significance = 211 Mismatches =
 190 Significance
211 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69. US-09-030-606-174 (1-1459)
US-09-020-747-74 Sequence 74, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative Substitutions
                         Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AAATGCCCAAATTGTATGGTGATAAAAGTCCCGT
520 530 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
378
25
       43
378
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1140 1150
GAAAATCAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Score
Residue Identity = Gaps
          11 11 1
initial Score
Residue Identity =
Gaps
```

Thu May

us-09-030-606-174.res

	570         580         600         610         620         630           GAGACAGAGACACACGGGCCGCATGGCGAGATGGAGACACACAC	640 650 660 670 680 690 700  GAGAGAGAAACTGAGAAACAGAGAATAAACACAGGAATAAAGAGAAGGAAG	710 720 730 740 750 760 770  CAGACATGGGGAGCACACACACACACACACACAGCATGGGCCTGAGGGC	790   840   820   830   840

| 850 | 860 | 870 | 880 | 990 | 900 | 910 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 

1440 1450 X TGTCTCAAAAAAAAAAAAAA

TTTACTACTAGTGAAACCC

1140 1150 GAAAATCAAGACT

70. US-09-030-606-174 (1-1459) US-09-020-747-10 Sequence 105, Application US/09020747

Optimized Score = 193 Significance = 0.12 Matches = 218 Mismatches = 305 Conservative Substitutions = 0 408 22 Initial Score Residue Identity Gaps

880 890 CATAAATAGTCGATT

06	1090 TACCCAGAG 	1150 ATCAAGACT         CTGAGCATT 0	1220 AGGCAGATC      GGGTGTCAC 310	1290 TACAAAAGT      TACGTGGAT 380	1360 TGCTTGAATA       AAAAGAAAAG	1430 GTAAGACTC         ATAATAATG
08	20         1030         1040         1050         1090         3.080         1090           GAAAAAATCCAAGTATAAGTGGCTTGTTCAAGGGTCAACTGTGTACCCAGAG         1	1100 1110 1130 1130 1130 1140 1150 1150 1150 1150 1150 1150 115	1160	1230 1240 1250 1260 1270 1280 1290 ACTTGAGGTAAGGAGTTCAAGACCAGCCTGGCCAAAATGGTGAAATCCTGTCTGT	1300 1310 1320 1330 1340 1350 1350 1360  TAGCTGGATATGGTGGCGCCTGTAATCCCAGCTACTTGGAGGCTGAGGCAGGAGAATTGCTTGAATA	1420 3GGCAACAGA 11   1 1ATTAAAAAA
. 70	GGTTGTTCAAGG GGTTGTTCAAGG 	AAA 	1200 CCAGCACTTTGGG                   CTTTAATTTTGTG	1270 GAAATCCTGTC 	1340 GGGAGGCTGAG   111 AAGGGGCGAGA 420	1410 TATACTCCAGCTGG           TTTCCTTTGCCAAG
09	50 1060 ATTCAAACCAGG   1   IGAACACCAATA: 130	1100 1130 1130 1130 1130 1130 1130 130	80 . 1190 ATGCCTGTAATCC 	1260 3CCAAAATGGT             TACTTAGTGAT	1330 CCCAGCTACTT 	1400 ATCACACCACT 
50	1050 GGACTTGTGCAT'           AGATATGTCTTG	1120   1120 	1180 GGTGGCTCATO       ATAAATTACTATO 260 27	1250 GACCAGCCTG( 	1320 CGCCTGTAATC       TTTCTCTTTC7 400	1390 GAGTTGAG2           CTATGGAAGG4
40	1040 AGTATAAGTGG 	1110 ICACAGATTCI        \TTTAAGATCI	1170 GGCTGGGCAGG       CTATTAGCAAA	1240 NGGAGTTCAA(         NCACATTCTG	1310 rGGTGGCAGG               \GTTGACAAG	1380 AGGTTGAAGT 
30	1020 1030 GAAAAATCCAA(         TCAAAGTGATCA(	1100 GGAAACAGTGF 	1160 CTACAAAGAGG         AAAAATCCACT 240 25	1230 ACTTGAGGTAA 	1300 TAGCTGGATA1   1	1370 TGGGAGGCAGA             GATTACGCATA

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us-09-030-606-174-inv.res

Page 1

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> 0 < O IntelliGenetics > 0 < O IntelliGenetics > 0 <
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FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file us-09-030-606-174-inv.res made by tport on Thu 1 May 103 15:03:07-PDT.

Query sequence being compared:US-09-030-606-174' (1-1459) Number of sequences searched:

Number of scores above cutoff: Results of the initial comparison of US-09-030-606-174' (1-1459) with:
 File: 6130043.seq
 File: 6252047.seq
 File: US08806596.seq
 File: US08904809.seq
 File: US09020747.seq
 File: US0904809.seq
 File: US0904809.seq
 File: US0904809.seq

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# Similarity matrix Unitary K-tuple Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group Onitary Mindow size 1 1 Joining penalty 5.00 Window size 1 Samdow size 1

PARAMETERS

4 30 500

#### SEARCH STATISTICS

Standard Deviation 15.60	Total Elapsed 00:00:01.00	
Median 33		189792 410 410
. Mean 32	CPU 00:00:01.00	Number of residues: Number of sequences searched: Number of scores above cutoff:
Scores:	Times:	Number o Number o Number o

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Initial Score =		88 Optimized Score	0	108	108 Significance - 3.59	3.59
Residue Identity =	39 39 30 30 30 30 30 30 30 30 30 30 30 30 30	39% Matches	•	128	Mismatches -	180
Gaps		20 Conservative Substitutions	stitut	ions	•	0

2. US-09-030-606-174' (1-1459) US-08-904-809-34 Sequence 34, Application US/08904809

Initial Score = 86 Optimized Score = 236 Significance = 3.46.

Residue Identity = 36% Matches = 280 Mismatches = 463

Gaps = 23 Conservative Substitutions = 0

  US-09-030-606-174' (1-1459) US-08-850-713-3 Sequence 3, Application US/08850713 Initial Score = 81 Optimized Score = 102 Significance = 3.14
Residue Identity = 41% Matches = 113 Mismatches = 155
Gaps = 6 Conservative Substitutions . . = 0

  us-09-030-606-174-inv

1070 1080 GCAGCACGGTAGGC

US/09020747 ' (1-1459) Sequence 174, Application 4. US-09-030-606-17 US-09-020-747-17

2.95 430 0 Significance Mismatches Optimized Score = 195
Matches = 194
Conservative Substitutions Initial Score Residue Identity Gaps

180

240 250 260 270 270 280 290 300 310 GATCTGCCTGCCTCGCCTCGCTTTGTAGAG | ||| | || || CAACTGTGTACCCAG

i' (1-1459) Sequence 30, Application US/08806596 US-09-030-606-174' 2.69 Optimized Score = · 240. Matches = 267 Conservative Substitutions 338 Initial Score Residue Identity Gaps

GGGC---AGAGGACCTCCTTGAAGAGGGCAGACACACCCGTGAGCTCACCGTTCGCCAGCAGACCCCAGC 1160

```
1340 1350 1360 1370 1380 1390 1400 GRACGGAGGCTCCAGCC
                                    cccccngggaaaagcggtttgcnttttngggggntccttccncttcccccccrcnctaanccctncgcctcg 680 690 700 710
CGGACACGGATTCGTCCAACTTGATGAGCATGAGGTCGTTAGCGAGCAAGGGTCTGTTGTACTCTGGGTGCC
```

(1-1459) Sequence 30, Application US/08904809 6. US-09-030-606-174 US-08-904-809-30 240 Significance = 267 Mismatches = Optimized Score = 240 Matches = 267 Conservative Substitutions 74 338 31 Initial Score = Residue Identity = Gaps

| 840 | 850 | 860 | 870 | 880 | 890 | 900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 | 1900 |

7. US-09-030-606-174' (1-1459) US-09-020-747-30 Sequence 30, Application US/09020747

2.69 Significance = Mismatches = Optimized Score = 240 Matches = 267 Conservative Substitutions 74 33<del>8</del> 31

cggccgcrgcrcrggcacarg 

| 10 | 720 | 740 | 750 | 760 | 760 | 750 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 |

---AGCTCCAGCTTTGTTCCNTTAATGAAG ANAACGGNCGCCACCNCGGTGGG-

8. US-09-030-606-174' (1-1459) US-08-806-596-10 Sequence 10, Application US/08806596 Initial Score = 72 Optimized Score = 253 Significance = 2.56
Residue Identity = 33% Matches = 270 Mismatches = 518
Gaps = 14 Conservative Substitutions = 0

  9. US-09-030-606-174' (1-1459) US-09-071-710-11 Sequence 11, Application US/09071710 Initial Score = 64 Optimized Score = 99 Significance = 2.05
Residue Identity = 40% Matches = 117 Mismatches = 155
Gaps = 14 Conservative Substitutions = 0

```
CTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCAACTTTNCCCTACCC 210 220
                                          920 930 940 950 960 X 970 980 cercagocorcectercacetrecages
                                                                             rctactctctctagga(
160
```

1010 STGGTACAGCG 990 1000 GCAGAACATGNTGGGG ' (1-1459) Sequence 11, Application US/09525397 10. US-09-030-606-174' US-09-525-397-11 Se Significance Mismatches 99 117 Conservative Substitutions Optimized Score Matches 64 408 14 Initial Score = Residue Identity = Gaps

11. US-09-030-606-174' (1-1459) US-09-841-894A-1 Sequence 11, Application US/09841894A

Significance Mismatches 99 Conservative Substitutions Optimized Score Matches 64 40**%** 14 Initial Score = Residue Identity =

US-09-030-606-174' (1-1459) US-08-904-809-66 Sequence 66, Application US/08904809 12.

2.05 182 0 11 B Significance Mismatches Optimized Score = 108
Matches = 123
Conservative Substitutions .64 38% 18 n # 11 Initial Score Residue Identity

13. US-09-030-606-174' (1-1459) US-09-020-747-66 Sequence 66, Application US/09020747

Optimized Score = 108 Significance Matches = 123 Mismatches Conservative Substitutions 64 38% 18 Initial Score Residue Identity Gaps

```
ACGCCTTTCCCTCAGAATTCAG
                    B0
                                      430 440 450 460 470 480 490 ACTTATACTTGGATTTTTAGGAGGGTTGCAACAATTTTAAAAAATTC
```

74' (1-1459) Sequence 1, Application US/09071710 14. US-09-030-606-1' US-09-071-710-1

Significance Mismatches Optimized Score = 96
Matches = 113
Conservative Substitutions Initial Score Residue Identity - Gaps

ccrecaerececcarcreceregrerrereres are ceregreeres and 110 120 130 130 140 150

GGCGTGGTGACAGCTTCAGCCGCCTT 240 250 X

950 ACGTT

US-09-030-606-174' (1-1459) US-09-525-397-1 Sequence 1, Application US/09525397

1.92 142 0 Significance Mismatches Optimized Score - 96
Matches - 113
Conservative Substitutions Initial Score Residue Identity Gaps

 GGCGGTGGTGACAGCTTCAGCCGCCTT 240 x

16. US-09-030-606-174' (1-1459) US-08-850-713-1 Sequence 1, Application US/08850713

 $\begin{array}{c} 1.92 \\ 142 \\ 0 \end{array}$ Significance Mismatches Optimized Score = 96
Matches = 113
Conservative Substitutions 62 42% 10 Initial Score Residue Identity Gaps

TCTGCCTCCCCATGTCTGTTTCTGTTTCTCTTTCTCTTTGCTTCTCTTTATTCCTGTGTTTATTTCTCTGTT 

```
ACAAGGGGGCATAATGAAGGAG
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGATTITCIATIGGGIGGAGGTCACCGCCCTCAGGCCCCA--TGCTGTIGGAAGGTCAACTGCATTICIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gggcrejáccággcgrecc
x 10 20
                                                                                                                                                                                    670 680 690 700 710 720 730
TATIGGIGGAGGICACCGCCCTCAGGCCCCATGCTGTTGGAAGGICAACTGCATTICTATGTGTGTGTTT
                                                                                                                                           1.92
492
0
                         Significance
Mismatches
                                                                                                                  Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                             1' (1-1459)
Sequence 47, Application US/08904809
                                                                                                     Sequence 1, Application US/09841894A
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative Substitutions
                                                                                                                  Optimized Score = 96
Matches = 113
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                 (1-1459)
                                                                                                                                                                                                                                                                                                                                                                                                   62 35%
                                                                                                                     428
10
                                                                                                                                                                                                                                                                                                                                                                                18. US-09-030-606-174'
. US-08-904-809-47 Se
                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score Residue Identity Gaps
                                                                                                  17. US-09-030-606-17.
US-09-841-894A-1
                                                                                                                   Initial Score Residue Identity Gaps
                                                                                                                                                                                                                                                                                                                                                       950
ACGTT
                                                                        950
ACGTT
                                                                                                                                                                                                                                                                                                               880
```

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CIGCTGCTTCAAATINTGCTCATTTACGACTATGGGACCTTGGGCAAGTNATCTTCACTTCTATGGGCN 710 720 730 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1300 1310 1320 1330 1340 1350 1360 1370 1370 10CTTAGGAGGGTGTGCTGCGTACGGAGAGGCTGCCTCCACCATCTGGCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 1240 1250 1260 1270 1280 1290
TGCGAAGCAATGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCCAACTTGATGAGCATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCCCTGATTCCCCACTCCTTAGAGGCAAGATAGGGTGGTTAAGAGTAGGGCTGGACCACTTGGAGCCAGG
610 610 620 630 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCACTCACCTCACCACACACATGGGAAGCCTTTCTGACTTGCTGATACTCCAGCATCTTGGAAC
520 530 540 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.92
492
                                                                                                                                                                                                                                                                                                                                                                             0 880 890 900 910 920 930 940 ceccaterectrecectrates
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 47, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
278
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US-09-020-747-47 Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
358
11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial Score
Residue Identity
Gaps
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4-inv.res

 1450 CAGTGTGCGGCTGACC

20. US-09-030-606-174' (1-1459) US-08-904-809-15 Sequence 15, Application US/08904809 Initial Score = 62 Optimized Score = 246 Significance = 1.92 Residue Identity = 35% Matches = 289 Mismatches = 494 Gaps = 37 Conservative Substitutions = 0 | 120 | 330 | 340 | 350 | 360 | 370 | 380 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 310 | 310 | 310 | 310 | 310 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390 | 390

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890 910 910 920 930 940 950 GENERAGICGCETCCCTCCCTTTCCCTTCTCACGTIGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 550 560 570 580 590 CCAACAAAGGTATTATGTTATTGGTAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAGGGGTGCCCAGAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 470 480 490 500 510 520 530 AATTTAGGAGAGATTGAGAAATTCACAGACGAACTGTGTAGGAAATTTCAAAAATT
                                                                                                                                                                                    CTCCCCTTCTCCACCCTTCCCTGAGTCGCCTGCCCTCCCCTTTCCCCTCTCTCACGTTGCAGGAGTCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \frac{1.92}{586}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 Significance = 346 Mismatches =
069
                                                                                                                                                                                                                                                                                                                                                                            950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ' (1-1459)
Sequence 15, Application US/09071710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative Substitutions
                                                                                               940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score
Matches
                                                                                                   930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
358
35
                                                                                                                                                                                                                                                         GCCCNAACCCNGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21. US-09-030-606-17
US-09-071-710-15
                                                                                                                  910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score = Residue Identity = Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200000 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1030
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750 760 770 780 790 800 810 CTCCCCAIGICIGITATICICIGITITATICICICICICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600 610 620 630 640 650 660 ccccgrcaacagarttrcraggartraggggagtcaaaaggt--ataagagartrtctatrg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 550 560 570 580 590 CCAACAAAGGTATTGTTATGTTATGGTAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 470 480 490 500 510 520 530
AATTTTAGGAGAGTTGCAACAATTTAAAAAATTCACAGACGAACTGTGTAGTAGAAATTCAAAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAGGGCGTGCCCAGAGCTGA X 20
                                                                                                                                                                                                                                                                     1180 1190 1230 1230 -----CCGTTCGCCAGCAGGCCAGCCAGCCAGGCAAGAGTTCCCCGGGGTAGGGCACTGC--GAAG
                                                                                                             TACGTGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGCCGGGCATCTGCCTGGACCTCGCCA
510 520 530 530
                                                                                                                                                                                                                                                                                                                                                                                                                                  \frac{1.92}{586}
                             1110 1120 1130 1140 1150 1160 1170 CTCTGGGTCAGGCCCCCGCGGGCAGGCCTCCTTGAAGAGGCCAGACACACCCCGTGAGCTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Significance = Mismatches =
                                                                                                                                                                                                                                                                                                                                                                GICCTCICCTCTCCCCAGICICTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTT 940 950
                                                                                                                                                                                                                                                                                                                                                                                                       22. US-09-030-606-174' (1-1459)
US-09-525-397-15 Sequence 15, Application US/09525397
                                                                                                                                                                                                                                                                                                                                                                                                                                     Optimized Score = 304
Matches = 346
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                        62
35%
35
                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score Residue Identity = Gaps
                                                                                                                                                                                                                                                                                                                                            X
CGGCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   670
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<i>,</i> •			•				•		
	•				<u> </u>				-
	#90 900 910 920 930 940 950.  ### GROUND ### F## GROUND ### GROUND	1040	<b>→                                    </b>	CCGTTCGCCAGCAGCCCAGAACGAGGCAAGAGTTCCCCGCGGTAGGCACTGCGAÀG	/30 740 750 760 770 780 790  1310 1320 1330 1340 1350 1360 1370  CGAGCAAGGGTCTGTTGTACTCTGGGTGCCGTACGGAGAGGCTCCCACCATCTGGCTCCTTGCTTT	1380	X CGGCTGACC       GTCCCTCTCTCTCCCCA( 940 950 96(	-09-030-606-174' (1-1459) -09-841-894A-1 Sequence 15, Application US/09841894A  1 Score	460 470 480 490 500 510 520 530

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600 610 620 630 640 650 660 CCCCGTCAACAGTATTCTAGTCAGGAGTCAAAAGTT--ATAAGAGGATTTCTATTG
                                                                                                                                                AGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGCTCGCCATTACTTTGCTACACAGGTAG 680 690 700 710 720
                                                                                                                                                                                                                                                                                                                                                                                                                                   AATITTAGGAGAGTTGCAACAATTTAAAAAATTCACAGACGAACTGTGTGTAGAAATATCAAAAATT
            ACCAGGGCGTGCCCAGAGCTGA
                               540 550 560 570 580 590 CCAACAAAGGTATATGATAAAAAGGTATGATAATGGTAAAGGCT
                                                                                                                                                                                                                                                                                                                                                820 830 840 850 860 870 880 CAGITICICICICICATCICICATCICCATCICCCATGCGGCCCIGI
                                                                                                                                                                                                                                                                                                                                                                                                                              1300
                                                                                                                                                                                                                                                                                                                                                                                                                             1280
                                                                                                                                                                                                                                                                                                                                                                                                                             1270
                                                                                                                                                                                                                                                                                                                                                                                                                              1260
                                                                                                                                                                                                                                                                                                                                                                                                                              1250
```

24. US-09-030-606-174' (1-1459) US-09-071-710-16 Sequence 16, Application US/09071710 Initial Score = 62 Optimized Score = 307 Significance = 1.92
Residue Identity = 35% Matches = 349 Mismatches = 591
Gaps = 35 Conservative Substitutions = 0

 | 880 | 890 | 900 | 910 | 920 | 930 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 9420 | 9430 | 940 | 9430 | 9420 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430 | 9430

25. US-09-030-606-174' (1-1459) US-09-525-397-16 Sequence 16, Application US/09525397 Initial Score = 62 Optimized Score = 307 Significance = 1.92
Residue Identity = 35% Matches = 349 Mismatches = 591
Gaps = 35 Conservative Substitutions , , = 0

<u> AGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGGTTCGGATGGGCAGCCTGGGGGCTGTTC</u>

 $\begin{array}{c} \mathtt{CTGCAGTGCGCCATCTCCCTTGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCA} \\ 100 & 110 & 150 & 160 \end{array}$ 

GGGCTGTACCAGGCCGTGCCC x 20

atcagaaaaattttaggagagttgcaacaatttaaaaaaattcacagacgaactgtgtagcttagaaatatc

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GCTCAGCCAGTCTGTCACTGCTATATGGTGTCTGCCGCAGGCCTGGTCTGGTCGCCATTTACTTTGCTAC 680 650 710 710 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GC -- GAAGCAATGCTGTCTCCGGATGGTGTCAGACTCGGACTGGATTCGTCCAACTTGATGAGCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 960 970 980 990 1000 1010 1020 ACGTTGCAGGAGTCCTTCTGGTCTTGCCCTCCGCCGCGCGCAGAACATGNTGGGGTGGTACAGCGGGGTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCTCCGTACGTGGTGGTGAGCCCACGAGGCCAGGTGGTTCCGGGCCGGGGCATCTGCCTGGA
510 520 530 540 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100 1110 1120 1130 1140 1150 1160 ACGCAGAGCTCTTGAAGAGGGCAGACACACCCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCAGGTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGGTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGGCCCCATCGTTTATGGGCTCCATTGTCCAGGCCCCATCGTTTATGGGCTCCATTGTCCAGGCCCCATCGTTTATGGGCTCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCCAGGCCCCATTGTCAGGCTCCATTGTCCAGGCCCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCCAGGCCCCATTGTCAGGCCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCAGGCCCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCATTGTCAGGCTCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCCATTGTCAGGCTCATTGTCAGGCTCATTGTCAGGCTCATTGTCAGGCTCATTGTCAGGCTCATTGTCAGGCTCATTGTCAGGCTCATTGTCAGGCTCAGTAGGCTCATTGTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1170 1210 1220 GCTCA-----CCGTTCGCCAGCAGACCAGAAACGAGGCAAGAGTTCCCCGCGGGTAGGGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 750 760 770 780 780 GTTTCTGCTTTGCTTTTGTTTTATTCTGTGTTTATTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
```

910

900

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ACGTTGCAGGAGTCCTTCTGGTCTTGCCCTCCGCCGGCGCAGAACATGNTGGGGTGGTACAGCGGGTCATAG
                     -----CCGTTCGCCAGCAGCCAGCCAGCAAACGAGGCAAGAGTTCCCCGCGGTAGGGCACT
                                                                                                                                                                                                                                                                                                                                                             1030 1040 1050 1060 1070 1080 1090 AGCTTANTGCAGACCTCNTCAGACACCACCGACACGTTCACGCACTGCAGCACGGTAGGCATTCTGCCTGGG
                                                                                                                                                                                   1240 1250 1260 1270 1280 1290 --GAAGCAATGCTGCGATGCTGGAGGATGGTGTCAGACTTGATGAGCATGAG
                                                                                                                            TGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGA
                                                                                                                                                                      1140
                                                                                                                                                                        1130
980
                                                                                                                                                                        1120
970
                                                                                                                                                                                                                                                                       GCTCA--
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ACAGTGTGCGGCTGAC

ecresescerecerer 940 ' (1-1459) Sequence 16, Application US/09841894A

26. US-09-030-606-17 US-09-841-894A-1

Initial Score Residue Identity Gaps

1.92 591 0

Significance Mismatches

Optimized Score = 307
Matches = 349
Conservative Substitutions

```
1.92
590
                                                                                                                        CCTCTCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGT x 960 980 1000
                                                                                                                                                                                 11 11
                                                                                                                                                                              Optimized Score = 308 Significance
Matches = 350 Mismatches
Conservative Substitutions
                                                                                                                                                         ' (1-1459)
Sequence 16, Application US/08850713
                                                                                                                                                                                Optimized Score
Matches
                                                                                                                                                                                   62
35$
                                                                                                     ×C
                                                                                                     1450
ACAGTGTGCGGCTGAC
                                                                                                                          geregegereerer
940
                                                                                                                                                           27. US-09-030-606-17
US-08-850-713-16
                                                                                                                                                                                Initial Score Residue Identity Gaps
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260 270 280 290 300 310 320
TCCCAAAGTGCTGGGGATTACAGGCATGAGCCAGCCTGCTTTTTTGTAGAGTCTTGATTTTTCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 130 140 150 160 170 180
TGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCTGCCACCATATCCAGCTAACTTTTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 240 250
ACAGACAGGATITCACCATTITGGCCAGGCIGGTCITGAACICCITACCICAAGIGAICIGCCIGCCICGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 50 60 70 80 90 100 110 GCCCCAGCTGGATATAGTGGTGTGATCTCAACTCACTTCAACCTCGCCTCCCATATTCAAGCAATTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANATTANTACAGTGTAATCTTT X 20
                                                                                                                                                                                                                                                                                                                                                                                                                    380 1390 . 1400 1410 1420 1430 . 1440
TGGTCGGCCTCAAGACTGTG----CAGGCCCAGCCCGATGGTGTGGAGCTCTGCACTCTGGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGG 730 740 750 750 760 770
                                                                                                                                                                                                                                                                                                                                                                      1310 1320 1330 1340 1350 1360 1370 GCGAGAGAGGCTCCACCATCTGGCTCCCTGGCTCT
                                                                                                                                                                                                      1170 1180 1190 1200 1210 1230 1230 1230 GIGAGCTCCCCGCGGGAGCCAGAACGAGGCAAGAGTTCCCCGCGGGTAGGGCACTGCGAA
                       TGTCTCCGTACGTGGTGGTGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGGCCGGGGCATCTGCCTGGA
1030 1040 1050 1060 1070 1080 1090
AGCTTANTGCAGACCTCNTCACGACACGACACGTTCACGCACTGCACGGTAGGCATTCTGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.86
508
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGGCGTCCTCTCTCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGGT 940 950 x 960 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 Significance 297 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28. US-09-030-606-174' (1-1459)
US-08-806-596-26 Sequence 26, Application US/08806596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Optimized Score = 247
Matches = 297
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
33%
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1450 X
AGTGTGCGGCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 H H
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Residue Identity
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-09-030-606-174-inv.re

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022 217 202 217 227 217 220 320 320 320 320	TCTCTTCGTGTTTCACCTCTATGAATCTGTGTCACTGTTTCCCTCTGGGTACACAGTTGACCTTGAACAAC	0	480 490 500 510 520 530 540  TTGCAACAATTTAAAAAAATTCACAGACGAACTGTGTAGCTTAGAAATTCCAAAAATTCCAACAAAGGTAT	550   560   570   580   590   600   610	620         630         640         650         660         670         680           CTATITCTAGGGAGTCAAAAGTTATAAGAGGATTTTCTATTGGGTGGAGGTCACCGCCCT         1   1   1   1   1   1   1   1   1   1	690         70         750           CAGGCCCCATGCTTGGAAGGTCAACTGCATTTCTATGTGTGTTTCTGCCTCCCCATGTCTGTTTCT         1           1	0	830   840   850   860   870   880   870   880   870   880   870	90   900   910   920   930   940   X   960   940   X   960   TCTCTGTCTCCCCTTTCCCCTTTCCCTTTCCCTTGCAGGA   11   1   1   1   1   1   1   1   1	970 980 990 GTCCTTCTGGTCTTGCCCTCCGCCGGCGCAGAACATGNT	US-09-030-606-174' (1-1459) US-09-020-747-17 Sequence 175, Application US/09020747	<ul> <li>61 Optimized Score = 369 Significance = 1.86</li> <li>348 Matches = 416 Mismatches = 749</li> <li>36 Conservative Substitutions = 0</li> </ul>	0 80 90 100 110 120 140 AACTCACTTCAACCTCCCAAGTATTCAAGCAATTCTCCTGCCTCCCAAGTAGCTGGGATTAC
330 . 3	TCTCTTCGTGT   CAGAGCANAC 230	400 410 CCTGGTTTGAA'        CCTGNACCGGG	480 TTGCAACAATT'               CTGCTTCAAGT 350	550 ATCATGAATGC       GCNCTGGGANC 410	620 CTATITCTAGE           AGCTCCCTGIE	690 700 CAGGCCCCATGCT 11 GGAATTTTNCCCT	760 770 GTTTCTCTTT- 	831 AG' L CNGNAANACNAAAA 690 700	890 900 TCTCTGTCTCCC                   TCTTTGCCTCTC 760 770	970 GTCCTTCTGGT	9. US-09-030-6 US-09-020-7	Initial Score Residue Identity Gaps	70 AACTCACTTCA

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TGCTGCACTGCGTGTCGCTGTCTGAGGANGTCTGCAGTAAGCTCTATGACCGCTGTACCACCACC 380 400 410 420 430 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 160 170 180 190 200 210 AGGCGCCTGCCACCATATCCAGCTTTTGCAGACAGATTTCACCATTTTGGCCAGGC
                                                                                                                                                          GTTTCCAGAACTCCTACACCATGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAGGGAGCCAGGGAGCCAGG 1100 110 120 130 140 150 150 160
                                                                                                                                                                                                                                    290 340 350 350 ccacctgcccagcctctttgtagagtcttgattttcctgtttctctttctgtgtagaatctg
                                                                                                                                                                                                                                                                        TGGTGGAGGCCAGCCTCTCCGTACGCCCCAGAGTACAACAGACTCTTGCTCGCTAACGACCTCATGCTCA
170 180 190 200 210 220 230
                                                                                                                                                                                                                                                                                                                                                                                                30 440 450 460 460 500 CTTGGATTTTTAGGAGAGTTGCAACAATTTAAAAAATTCACAGACG
                                                       TGGTCATGGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACT
                                                                                                                                                                                                                                                                                                                                                          360 370 380 390 400 410 420 TGTCACTGTTTCCTTGGTTACACCTTTTTACTACTTTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------AGAATGCCTACCG
360 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 520 530 540 550 560 570 ACTGTGGTAGCTTAGAAAAATTCCAACAAAGGTATATCATGAATGCATAAAACGTATGCATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 730 740 750 760 770 . 780 780 CATTTCTATGTGTGTTTCTGTTTCTTTGTTTGTTTATT
                                                                                                                  220 230 240 250 260 270 280 TGGTCTTGAACTCCTTACCTCAAGTGCTTGCGATTACAGGCATGAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGGAACTCTTGCCTCGTNTCTGGCTGGGGTCTGCTGGCGAACGGC 320 330
                                                                              9
```

1050

1030

TAGGGCACTGCGAAGCAATGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCCAACTTGATGA

940 950 960 970 980 990 1000 recerrrecerrecerrecerrecerrenged ATCTTTTTTACTTTTGTAAAAGCTTATGCTCTTTGGTATCTATATCTGTGAAAGTTTTAATGAT-CTGCCA 100 110 150 150 1010 1020 1030 1040 1050 1060 1070 TGGTACAGGGGGTCATAAAGAGCTTAANTGCAGACCTCNTCAGACACCACCGACACGTTCAGGCACTGCAGCACG AGAAACCAGTATCTCTNAAAAC X 20 TGCGGCCCTGTGTGTCTCTGTCTCCCCTTCTCCACCCTTCCCTGAGTCGCCTGCCC 1.80 263 0 910 Optimized Score = 129
Matches = 150
Conservative Substitutions 60 35% 10 790 800 TCCTGTGTTTATTTC CTCTGCATCTCGCCA Initial Score Residue Identity Rans Gaps

80 780 740 750 720 730 740 750 caccecercargetetregrands caccecercargeterregrands caccecerate caccerate caccecerate caccecerate

830 840 TCTCTAGTTGTCACTGTCTCTCT 32. US-09-030-606-174' (1-1459) US-08-904-809-5 Sequence 5, Application US/08904809 Initial Score = 58 Optimized Score = 280 Significance = 1.67
Residue Identity = 38% Matches = 322 Mismatches = 502
Gaps = 20 Conservative Substitutions = 0

780

33. US-09-030-606-174' (1-1459) US-09-020-747-37 Sequence 37, Application US/09020747 Initial Score = 57 Optimized Score = 158 Significance = 1.60
Residue Identity = 33% Matches = 178 Mismatches = 350
Gaps = 7 Conservative Substitutions = 0

X CGGCTGACC

```
GGGGAAANAAACCCGGCNGNGANCCNCCTTGTTTGAATGCNAAGGNAATAATCCTCCTG
530 540 550 560
```

34. US-09-030-606-174' (1-1459) US-08-806-596-5 Sequence 5, Application US/08806596 Initial Score = 57 Optimized Score = 280 Significance = 1.60 Residue Identity = 38% Matches = 322 Mismatches = 502 Gaps = 20 Conservative Substitutions = 0

| 80 | 90 | 100 | 110 | 120 | 130 | 140 | 120 | 130 | 140 | 140 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |

 35. US-09-030-606-174' (1-1459) US-09-020-747-5 Sequence 5, Application US/09020747 Initial Score = 57 Optimized Score = 280 Significance = 1.60
Residue Identity = 38% Matches = 322 Mismatches = 502
Gaps = 20 Conservative Substitutions = 0

 | 340 | 350 | 350 | 350 | 350 | 340 | 350 | 350 | 340 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350 | 350

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acctcaagtgatctgcctgcctcgcctcccaaagtgctgggattacaggcatgagccaccctgcccagcctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial Score = Residue Identity = Gaps = =
                                                                                                         160 170 180 190 200 210 220 ATCCAGCTAACTTTTGTATTTTAGTACAGACAGGATTTCACCATTTTGGCCCAGGCTGGTCTTGAACTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670 680 690 700 710 ---TTTCTATIGGTGGAGGTCACCCCCTCAGGCCCCATGCTGTTGGAAGGT
                                        ACTCGTTGCANATCAGGGGCCC X
                                                                                                                                                                                                                                                                                                                                                                                                        TCCCCTCTCTCACGTTGCAGGAGTCCTTCTGCCCTCCGCCGCCGCAGAACATGNTGGGGTGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTCTATNTGGCCAGTGTGGC X
                                                                                                                                                                                                                                                                                                                                                                                                                              Significance
Mismatches
                                                                                                                                                                                                                                                                                              Significance
Mismatches
                                                                                                                                                                                                                                                             ' (1-1459)
Sequence 120, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37. US-09-030-606-174' (1-1459)
US-08-904-809-10 Sequence 10, Application US/08904809
                                                                                                                                                                                                                                                                                              Optimized Score = 62
Matches = 67
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimized Score = 253
Matches = 270
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1030 1040 1050
TANTGCAGACCTCNTCAGACACCGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAGCCCTGCAGATCCTGCCCTACAC---0 120
                                                                                                                                                                                                                  860 870 880 TCCATCTGCATCTCTGTGTG
                                                                                                                                                                                                                                                                                              56
738
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCGGGTTCACCTTCT
                               CAAAAGTTATAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1020
GCGGGTCATAGAGCT1
                                                                                                                                                                                                                                                             36. US-09-030-606-1
US-09-020-747-1
                                                                                                                                                                                                                                                                                          Initial Score Residue Identity Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Score Residue Identity Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                   650
                                                                                                                                                                                                                                                                                                                                                                                                           940
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TGTTTCTCTCAGTTCTCTCTCTCAGTGTCACTGTCTCCCTGTGTCTCTCCCATCTCGCCATG
                                                                                                     GCTGTCCCANGTGGCCCCATCCCTGTTTATGGCCTCCATTGTCCAGCTCAGCTAGTCACTGCCTATAT

450 460 470 510 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGTCTGCCGCAGGCTGGGTCTGGTCCCATTTACTTTGCTACACAGGTANTATTTGACAAGAACGANTTG 520 520 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTCCTGTTAACCCCATGGGGCTGCCGGCTTGGCCGCCAATTTCTGTTGCTGCCAAANTNATGTGGCTCTC
660 670 680 690 700 700
380 390 400 410 420 420 440 440 GGGTACACAGTTGAACACCCTGGTTTGAATGCACAAGTCCACTTATATACTTGGATTTTTTCAATA
                                                                                                                                                                                                                                                                            450 460 470 480 490 500 510 AACACATTTAAAAAATTTAAAAAATTTAGAA
                                                                                                                                                                                                                                                                                                                             AGCCCACCGANGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCTTCCT 370 380 430 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 750 760 760 700 700 770 780 790 800 rGTTTCTGCTCTCTTTATTCCCCATGTTTATTATTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 30 40 50 60 x 70 80 TITITGAGAGACAGAGTCTCAACTCCAGCTCTCAACCTC
                                                                  310 320 330 340 340 350 370 TTTGTAGAGTCTTGTGTGTTTCCCTCT
                                                                                                                                                                                                                                                                                                                                                                                    520 530 540 580 ATATCAAAAAATTCATGAATGCATAAAACGTATGCATAAATCGACTATTATGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGTCTATNTGGCCAGTGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 100 110 120 130 140 150 TGCCTCCCAAGTAGCTGGGATTACAGGCCCCTGCCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.54
518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGCCACCTGTTGCTGGCTGAAGTGCNTACNGCNCANCTNGGGGGGTNGGGNGTTCCC 740 750 780 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38. US-09-030-606-174' (1-1459)
US-09-020-747-10 Sequence 10, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score - 253
Matches - 270
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     880 890 900 910 GGGCCCTGTGTCTCCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338
14
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39. US-09-030-606-174' (1-1459) US-09-020-747-75 Sequence 75, Application US/09020

Initial Score = 55 Optimized Score = 166 Significance = 1.47
Residue Identity = 36% Matches = 172 Mismatches = 295
Gaps. = 6 Conservative Substitutions = 0

40. US-09-030-606-174' (1-1459) US-08-806-596-17 Sequence 17, Application US/08806596

Initial Score = 55 Optimized Score = 230 Significance = 1.47 
Residue Identity = 34% Matches = 269 Mismatches = 466 
Gaps = 38 Conservative Substitutions = 0

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650 660 710 710 AAAGTTATAGGGTGGAGGTCACCGCCTCAGGCCCCATGCTGTGGAAGGTCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 330 340 350 350 CCTGCCCAGCCTTTTTCTCTGTTTCTCTTTCACCTCTATGAATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 370 380 390 400 410 420 retreacted transfer and trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 520 530 540 550 560 570 AACTGTAGAAATTCCAACAAAGGTATATCATGAATGCATAAAACGTATGCATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 20 30 X 40 50 60 70 TTTTTTTTTTTTTTGAGACAGAGTCTTACTCTGTTGCCCCAGCTGGAGTATAGTGGTGATCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGTATTTTCTGTAAGATCAGGTGTTCCTCCTCG x 10 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 580 590 600 610 620 630 640 TCGACTATTTATGTTATTTTTGGGGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGGGANCCCATATCTCNACCANTACTCACCNTNCCCCCCNTGNNACCCANCCTTCTANNGNTTCCCNCC 600 610 620 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.35
493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Optimized Score = 232 Significance Matches = 256 Mismatches Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42. US-09-030-606-174' (1-1459)
US-09-020-747-40 Sequence 40, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
33%
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U E
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750 x
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Residue Identity
Gaps
```

| 80 | 90 | 100 | 110 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |

   43. US-09-030-606-174' (1-1459) US-09-020-747-11 Sequence 115, Application US/09020747 Initial Score = 52 Optimized Score = 122 Significance = 1.28 Residue Identity = 36\$ Matches = 141 Mismatches = 225.

| 700 | 710 | 720 | 730 | 740 | 750 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760

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44. US-09-030-606-174' (1-1459) US-08-904-809-46 Sequence 46, Application US/08904809 Initial Score = 52 Optimized Score = 198 Significance = 1.28 Residue Identity = 34% Matches = 207 Mismatches = 382 Gaps = 3 Conservative Substitutions = 0

74' (1-1459) 5 Sequence 46, Application US/09020747 45. US-09-030-606-17 US-09-020-747-46

Optimized Score = 198 Significance Matches = 207 Mismatches Conservative Substitutions Optimized Score Matches 348 348 Initial Score Residue Identity Gaps

530 500

46.

US-09-030-606-174' (1-1459) US-08-806-596-16 Sequence 16, Application US/08806596

1.28 498 257 Significance = 284 Mismatches = Optimized Score = 257
Matches = 284
Conservative Substitutions 52 35% 15 Initial Score = Residue Identity = Gaps

CACCCACGGTGACTGCATTGGATGTCATACAAAAGCTGATTGAAGCAACCCTCTACTTTTGGTCGT 

 47. US-09-030-606-174' (1-1459) US-08-904-809-16 Sequence 16, Application US/08904809 Initial Score = 52 Optimized Score = 257 Significance = 1.28
Residue Identity = 35% Matches = 284 Mismatches = 498
Gaps = 15 Conservative Substitutions = 0

 48. US-09-030-606-174' (1-1459) US-09-020-747-16 Sequence 16, Application US/09020747 Initial Score = 52 Optimized Score = 257 Significance = 1.28
Residue Identity = 35% Matches = 284 Mismatches = 498
Gaps = 15 Conservative Substitutions = 0

 | 700 | 710 | 750 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760

1370 350 1340

' (1-1459) Sequence 133, Application US/09020747 49. US-09-030-606-1 US-09-020-747-1

Significance Mismatches Optimized Score = 99
Matches = 120
Conservative Substitutions 51 40% 22 Initial Score Residue Identity Gaps

CCTTGAACAACCCTGGTTTGAATGCACAAGTCCACTTATACTTGGATTTTTTCAATAAACACATCAGAAAAA 

TCAACAGTAGGCTATTTCTAGTCAGGTTTTTGGGGAGTCA

US-09-030-606-174' (1-1459) US-09-020-747-17 Sequence 171, Application US/09020747

1.22 783 0 Significance - Mismatches -396 445 Conservative Substitutions Optimized Score Matches 51 35% 30 Initial Score Residue Identity

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Number of sequences searched:
Number of scores above cutoff:
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US-09-020-747-17 Sequence 175, Application US/09020747
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590	AGGTGTCTP 	640 660	ACTGGGAAC	ACTGGGAAC 710	730		TCCTCCCTC 780
580	TACTTGCAGGGCCTTGTGTTTTCGGAAAAGCCCCGTGTGGCCAACTTGGCGTGCCAGGTGTCTACACCAAC	630	CTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGNCCAGTTAACTCTGGGGACTGGGAACCCATGAA	CTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAA 50 700 710 720	720	ATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATATCTGTTCCCAGCCCCTCCTCCTCAGGCCCA 	ATTGACCCCCAAATACATCCTGCGGAAGGAATTCAGGAATATCTGTTCCCAGCCCCTCCTCCTCAGGCCCA 730 730 730 780 750 750 750 750
570	TGTGGCCAAC           TGTGGCCAAG	620	CAGNCCAGTT	CAGGCCAGTT 690	710	GAATATCTGT	GAATATCTGT 760
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540	AGGGCCTTG	590 610	AATTCACTG	AATTCACTGI 660	680	CCCAAATAC	CCCAAATAC
530	TACTTGC	009	CTCTGC#	CTCTGC2 650	670	ATTGACC	ATTGACC

| 750 | 760 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810 | 810

 

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3. US-09-030-606-175 (1-1167) US-09-020-747-17 Sequence 173, Application Initial Score - 794 Optimized Score - 1117 Significance = 12.43
Residue Identity - 90% Matches - 1137 Mismatches = 30
Gaps - 83 Conservative Substitutions = 0

| 10 | 780 | 790 | 800 | 810 | 820 | 830 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 |

us-09-030-606-175.res

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SAGGAGTCCAGCCCTCCTCCNTCAGACCCCAGGACCCCCCCCCC	930 940 950 960 970 980  5TGCAGGCCCCAACCCTCNTCCNTCAGAGTCAGAGGCCCCCAACCCCTCGTTCCC  11	990 1000 1010 1020 1030 1040 1050  CAGACCCAGAGGTCCCAGCCCTCCTCCTCAGACCCAGCGGTCCAATGCCACTAGANTNTCCCT	100	0 1140 1150 X TAGATCCAGAAATAAAGTNTAAGAGAGCGCAAAAAA 	-606-175 (1-1167) -747-17 Sequence 177, Application US/09020747	483 Optimized Score = 592 Significance = 7.34  ity = 55% Matches = 638 Mismatches = 472  2 Conservative Substitutions = 0	x         10         20         30         40         50         60           GCGCAGCCTGGCAGCGCATGGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGAT	70 80 90 100 110 120 130 CCGCAGTGTGTTTCCAGAACTCCTACACCATCGGGCTGGGCTGCACAGTCTT	150	220 230 240 250 260 270 280  CTCTTGCTCGCTAACGACCTCATCATGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGC	300 320 320 340 350  TGCTTCGCAGTGCCTACCGCGGGGAACTCTTGCCTCGTNTCTGGCTGGGTCTGCTGGCGAAC	360       370       390       400       410       420         GGCAGAATGCCTACCGTGCTGGTGTCGGTGTCTCGGGANGTCTGCAGTAAGCTCTAT       1	430 440 450 460 470 480 490 GACCCGCTGTACCACCCAGCATGTTCTGCGCCGGGGGGAGACCAGAAGGACTCCTGCAACGTGAC
CCTCAGACCCAGGA 940	920 GACCCAGGGGTGCAG 	990 CAGACCCAG           CAGACCCAG	1060 GTACACAG7          GNACACAG7	1130 1.7 TAGATCCA(                   TAGATCCA( 1230	4. US-09-030 US-09-020	Initial Score Residue Identity Gaps	X GC GCGCACTC X	70 CCGCAGTG          CCGCAGTG	140 150 GAGGCCGACCAGGA : [           GAGGCCGACCAAGA 150 1:	CTCTTGC1             CCCTTGC1	290 ATCAGCATTGCTTCO 	360 GGCAGAA?       GATGCTG?	430 GACCCGC

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| 190 | 840 | 850 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 
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644 Mismatches
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US-09-020-747-17 Sequence 174, Application US/09020747
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Matches = 644
Conservative Substitutions
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GGAAAACGAATTGTTCTGCTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACTGTTTCCA
110 120 130 140 150 160  GAA
170
240         250         260         270         280         300           GCTCATCAAGTTGGACTCGGAGTCTGACACCATCGGAGCATTGCTTCGCAGTGCCC         111111111111111111111111111111111111
310 320 330 340 350  TACCGCGGGGAACTCTTGCCTCGTNTCTGGCTGGGGTCTGCTGGCGAAC
360
370         380         400         410         420         430           ACCGTGCTGCAGTGAGGTGTCTGAGGANGTCTGCAGTAAGCTCTATGACCCGCTGTAC
40         450         470         480         490           CACCCCAGCATGTTCTGCGCGGGGGGGAGGCCAGAAGGACTCCTGCAACGGTGACTCT         1         1
510 520 530 540 550 560 570  GGGGGGCCCTGATCTGCAACGGCTTTGTGTCTTTCGGAAAAGCCCCGTGTGCCAACTT
580         600         610         620         630         640           GGCGTGCCAGGTGACCTCTGCAAATTCACTGAGGAAAACGGTCCAGNCCAGTTAA
650 660 670 680 690 700 710  CTCTGGGGACTGGGAATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATATCTGTTC  1 11   1   1   1   1   1   1   1   1
CCAGCCCCTCCTCCTCAGGCCCCAGGCCCCCAGCCCTCCTCAAACCAAGGGTACAGATC

790 800 CCCA-GCCCTCCTCC

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TTGACTCCCCAAAAAACCTGAAATAGCCTACTGTTGACGGGGAGCCTTACCAATAACATAAATAGTCG 820 850 870 ...880
                                    ATTIATGCATACGTTTATGCATTCATGATATACCTTTGTTGGAATTTTTTGATATTTCTAAGCTACACGT 890 940 950
                         3.24
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                                                                                                                                                                                                                                                            Significance
Mismatches
                                                                                                                                                                                                                                         US-09-030-606-175 (1-1167)
US-08-904-809-45 Sequence 45, Application US/08904809
                                                                                                                                                                                                                                                           Optimized Score = 233
Matches = 230
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                         450 460 470 480 CCCCAGCATGTTCTGCGCCGGCGGAGGCCAAGAAGAAGGACTCC
                                                                                                                                                                                                                 CAGCCTGGCCAAAATGGTGAAATCCTGTC 1250 1250 1260.
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98%
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                                                                                                                                                                                                                                                             Score
Identity
                                                                                                                                                                                                                                                           Initial &
Residue 1
Gaps
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950 960 970 980 990 1000 1010 TCAGAGTCAGAGGTCCCAAGCCCTCCTCC 240 250 260 270 280 290 300 TCATCAAGTTGGACGTCCGAGTCTCGCAGTCCCTA TCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTT 170 180 190 200 210 220 230 230 GATGGTGGAGGCCAGCCTCTCCGTACGGCACCTCATGC X 10 20 GCGCAGCCTGGC--AGGCGGC CGTGCTGCACTGCGTGAACGTGTCGGTGTCTGAGGANGTCTGCAGTAAGCTCTATGACCGCTGTACCA ACAACAGACCTTGCTCGCTAA x 10 20 160 170 180 190 200 X 210 220 GCCAGGGAGGCCAGAGGAGGCCAGGCCAGCCTCTCCGTACGGCAGCCAGACTACAACAGACTCTTGCTCGCTAAA 0.85 700 0 3.24 4 0 Matches 410 Significance Matches 453 Mismatches Conservative Substitutions Significance Mismatches US/09020747 US/09020747 Optimized Score = 233
Matches = 230
Conservative Substitutions 450 460 470 480 ccccagcatgttctgcgcgggggggggggaggccaggaggactcc (1-1167) Sequence 109, Application Application Sequence 45, (1-1167)233 98% 0 8. US-09-030-606-175 US-09-020-747-10 7. US-09-030-606-175 US-09-020-747-45 rcrcrcrcrcrch 590 Initial Score = Residue Identity = Gaps 320 Initial Score = Residue Identity = 380 310

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        920
        930
        940

        GACGCAGCACCCCCAGCCCCAGCCCCCCCCCCCCCCTCNTCCN
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ACCICIGCAAAITCACIGAGIAGGAAAACGICCAGNCCAGITAAACICIGGGACIGGGAACCCAIG
                                                                                                                                                                                                                                                                                                                                                                                         AATTCCACTCTCGCCCGCCTCTTTATCGTCATCTCCCACTTGCGCCTCTGCGCAAT 730 740 750 760 760 770 780 790
                                                                                                                                                                                                                                                                                                                                530 540 550 560 570 580 590 GGIACTTGCGGAAAAGCCCCGTGTGGCCAACTTGGCGTGCCAGGTGTCTACACCA
CCGCGGGGAACTCTTGCCTCGTNTCTGGCTGGGGTCTGCTGGCGAACGGCAGAATGCCTACCGTGCTGCACT
                                               acacatteggeaagtacaggeaacage-datetetactggaaggedeagggtade--geeteateggg
660 710 720
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Thu May

9. US-09-030-606-175 (1-1167)
US-08-806-596-16 Sequence 16, Application US/08806596

Initial Score = 85 Optimized Score = 259 Significance = 0.82 Residue Identity = 34% Matches = 283 Mismatches = 518 Gaps = 27 Conservative Substitutions = 0

   780

10. US-09-030-606-175 (1-1167) US-08-904-809-16 Sequence 16, Application US/08904809 Initial Score = 85 Optimized Score = 259 Significance = 0.82 Residue Identity = 34% Matches = 283 Mismatches = 518 Gaps = 27 Conservative Substitutions = 0

 CAGCCTCTCCGTACGGCACCCAGAGTACAACAGACTCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGGA

220

210

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 640
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 CACTGAGTGATAGAGAAAACGTCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCA

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| 830 | 840 | 850 | 860 | 870 | 880 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890

11. US-09-030-606-175 (1-1167) US-09-020-747-16 Sequence 16, Application US/09020747 Initial Score = 85 Optimized Score = 259 Significance = 0.82 Residue Identity = 34% Matches = 283 Mismatches = 518 Gaps = 27 Conservative Substitutions = 0

 | 250 | 260 | 310 | 320 | 320 | 310 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320 | 320

| 830 | 840 | 850 | 860 | 870 | 880 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890

900 x 920 930 940 950 960 CAGCCCNTCNTCAGAGTCAGAGG GAGCCCCTCNTCAGAGTCAGAGG GAGCCCCTCNTCCNTCAGAGTCAGAGG GAGCCCCTCNTCCNTCAGAGTCAGAGG GAGCCCCCTCNTCCNTCAGAGTCAGAGG GAGCCTCCTGCCCCNG 900 800

12. US-09-030-606-175 (1-1167) US-08-904-809-21 Sequence 21, Application US/08904809 Initial Score = 73 Optimized Score = 209 Significance = 0.62
Residue Identity = 31% Matches = 245 Mismatches = 507
Gaps = 29 Conservative Substitutions

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230	10   600   610   620   630   640   650	60         610         680         690         700         710         720         730           GAACCCATGAAATTGACGGAATACCTCCTCCTCCTC         I         <	740 750 760 770 780 790 800 CCTCAGGCCCAGGCCCCCCCCCCCCCCCCCCCCCCCCCC	### ### ### ### ### ### ### ### ### ##	880         890         900         910         920         930         940           AGACGCAGGACCCCCCAGCCCNTCNTCCGTCAGACCCAGGGCTGCAGGCCCCCAACCCCTCNTCC         1   1   1   1   1   1   1   1   1   1	950         960         970         980         1010         1010           NTCAGAGTCAGAGCCCCAACCCCTCGTTCCCCAGACGTNCAGGTCCCAGCCCTCCTC         1	20         1030         1040         1050         1090         1090           CCTCAGACCCAGGGGCCCCTAGTGGGCANGTTGACCCA           I
220	640 CCAGNCCAG1       CCCTCCCCC	710 GGAATATCTC     ICCTAAACTC?	780 .AAGGGTACAC 	ACCCAGGAGTC ACCCAGGAGTC A	930 GGGTGCAGGCC           NTTTTGGTTCC	1000 AGAGGTNCAC       TGGNTTCNNC	1070 GTGCCCCTT      AACCCCGGC
210	630 AGAAAACCGI NCCCCCTANC 280	700 AANGAATTCA       AAGTCNCNCN 350	770 CCCTCAAACC        AACTCAAAAA	840 CNTCCNTCAGA         GGTCCNTNAAN	920 TCAGACCCAGG         ACAGCATI	990 CCCCAGACCC             TCGGTTANCC	1060 CCTGTACACAC
200	620 TGAGTGGATAG 11   CGATTACCCNT 270	690 ACATCCTGCGG        AGNTCCCCNNC, 340	760 CAGCCCCTCCT- 111 1 TCACCCTACTC 410	830 8 CCCAGCCCCTC   CTATTTAGNG 480	CCCNTCNTCCG1 CCCNTCNTCCG1 CCCNTCNTCCG1 540	980 AACCCTCGTT       CNTCTTTTCCT 610	20 1030 1040 1050 1 CCTCAGACCCAGGGTCCAATGCCACCTAGANTNTCCCT 
190	610 AAATTCAC'             TTTCCTNANC' 260	680 SACCCCCAAAT               SNCNCCCGCT	750 srccaggcccc          srccccgaarc 400	820 AGTCCAGACCC           IGACTGGGTCT 470	890 . 900 CAGACCCCCAGCC           CAATTTCCNAANGC	970 rccaagccccc   11 rngaacggcrv 600	1040 STCCAATGCCA(1   1   1   1   1   1   1   1   1   1
. 180	600 AACCTCTGC/       NNCANATGA1	670 CATGAAATTC       NAAGGNNGCC	740 GGCCCAGGAC 	810 AGACCCAGGI      TNACAC-TNI 460	0 CAGGAGTCC! 	960 AGTCAGAGGI 	1030 GACCCAGCGC I TTTAAATTCN 660
170 .	590 ACACC TNNNC 240	660 GAACCO   11   11   GGNCCO	CCTCA   1   CNTGA	CCCTC   GNTTA	880 AGACGC	950 NTCAG   1 NGAAT	1020 CCTCA 11 CCCNT

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75 (1-1167) Sequence 3, Application US/08806596 13. US-09-030-606-17 US-08-806-596-3

0.49 Significance Mismatches Optimized Score = 259
Matches = 302
Conservative Substitutions 65 38% 17 Initial Score
Residue Identity = Gaps

ACCCCCACNTNNACCGCTTACACTTTGCCAGCGCCTTANCGCCCGCTCCCTTTCTTCTTCCTTTCTTCCTT 720 730

CCTCCTCCNTCAGACGCAG

US-09-030-606-175 (1-1167) US-09-020-747-3 Sequence 3, Application US/09020747

0.49 464 0 Significance Mismatches Optimized Score = 259
Matches = 302
Conservative Substitutions 65 38% 17 Initial Score Residue Identity Gaps

740 750 760 770 780 790 CAGGCCCAGGAGCCCCAGGAGCTACAGGTACAGGTACAGGTACAGATCCC GCCAGGTGTCTACCACCAACCTCTGCAAATTCACTGAGT - - - GGATAGAAAAACCGTCCAGNCCAGTTAACT CTTGCAGCACATCCCCTTTCGCCAGCTGGGCGTAANCGAAAAGGCCCGCACCGATCGCCTTCCAACA 520 530 540 550 550 650 660 670 680 690 700 710 CTGGGGAACGCAATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATACTGTTCCC 230 240 250 260 270 280 290 AACGACCTCATC-AAGTTGGACGAATCCGTGTCCGAGTCTGACCATCCGGAGCATCAGCATTGC 300 310 320 330 340 350 360 TCGCAGGGGGAACGGCAGATGCC 160 170 180 190 200 210 220 GAGCCAGGCAGCCTCGTACGAGGCAGCAGACAGACTTTGCTCGCT GGGTGTTTAACAGCAGAGGTGCGGGGGCTC--ACGTCCTGCTCCTCGTGATAAACGAGCCCCG 30 40 50 50 640 610 009 TrccrrcrrcrcArcA 730 580

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320 330 340 350 360 370 380 390 CTGGCGTGCTGCGTGCGTGCGTGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 190 200 210 220 X 230 240 CCAGCCTCCCTACCTCCCTACCACCTCATCACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cccacccracccaaararraga
                                                                                                                                                                                                                                                                                                                            240 250 260 270 280 290 300 310 TCAAGTIGGACGAGTCCGIGTCCGAGTCTTCGCAGTGCCCTACCG
                                                                                                                                                                                                                                                                                                                                                      30 40 50 60 70 80 90 TGGTCATGGTCATGGTGCATCCGCAGTGGTGTGTCAGCCGCACAT
                                                                                                                                                                                                  x 10 20
GCGCAGCCCTGGCAGGCGGCAC
                                                                                                    320 X 330 340 350 360 370 CGGGGAACTCTTGCCTGGCTGGCTGCTGCTGCCAGAATGCCTACCGTGCTGC TGCTGCGAAACGGCAGAATGCCTACCGTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score = 253 Significance = 288 Mismatches = 200 Mismatches = Conservative Substitutions = -
                          Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16. US-09-030-606-175 (1-1167)
US-08-904-809-11 Sequence 11, Application US/08904809
15. US-09-030-606-175 (1-1167)
US-09-020-747-84 Sequence 84, Application US/09020747
                             Optimized Score = 115
Matches = 113
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
36%
21
                                 64
348
0
                                                                                                                                                                                                                                                                                                                                                                                                                                     TINCCGCCTCATCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial Score = Residue Identity = Gaps = =
                                    Score
Identity
                                   Initial
Residue
Gaps
```

CCTCCTCCNTCAGA

| 540 | 550 | 560 | 570 | 580 | 590 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600 | 600

17. US-09-030-606-175 (1-1167) US-08-904-809-23 Sequence 23, Application US/08904809 Initial Score = 61 Optimized Score = 252 Significance = 0.4
Residue Identity = 33% Matches = 29% Mismatches = 55
Gaps = 37 Conservative Substitutions =

   | 810 | 820 | 840 | 850 | 850 | 840 | 850 | 840 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850

 

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GACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACCGCGGGGAACTCTTGCC---TCGTNTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgencectificendecedece x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 140 150 160 170 X 180 190
GGCCTGCACAGGCCGACCAAGAGCCAGGAGGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATAATTCTAACATCCTGGAGAAAATGGCAGTTTGACCGAACCTGTTCACAACGGTAGAGGCTGATTCTA

290 310 310 320 330
                                                                                                                                                                                                                     280 340 300 310 320 340 340 TCCGGAGCATCATGCTTGCTTGCTTGGCTGGGGTCTGC
                                                                                                                                                                                                                                                                                                                                      350 360 410 410 TGGCGAGAACGCCAGAATGCCTACCGTGCTGCTGTGTCTGAGGANGTCTGCAGTA
                                                                                                                                                                      Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     s (1-1167)
Sequence 36, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score = 256
Matches = 302
Conservative Substitutions
                        Optimized Score = 124
Matches = 139
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                     ACGAAACTTGTAGAATGAAGCCTGGA
360 370 380
(1-1167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
35%
36
                                                                                                                                                                                                                                                                                                                                                                                                                                     19. US-09-030-606-175
US-08-904-809-36
18. US-09-030-606-175
US-09-020-747-16
                                                                 X
GCGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial Score Residue Identity Gaps
                           Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                    420
AGCT
```

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x 10 20
GCGCAGCCTGGCAGGCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATAATCCTNGAACCATGGTGCCTTCCGGTCTGATCCNAAAGGAATGTTCCTGGGTCCCANTCCCTCTT 620 630 630 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990 1000 1010 X 1020 1030 1040 1050 cccagacccagaggtccaatgccacctagantntcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 780 790 800 810 820 830 CCTCABACCAAGGATCCAGACCCCCCTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCNTCAGACCCAGGAGTCCAGCCCCTCCTCCTCCTTCAGACGCAGGAGTCCAGACCCCCAGCCCCTCTTCAGACGCAGGAGTCCAGACCCCCAGCCCCAGCCCTTCTTCAGACGCAGGAGTCCAGACCCCCAGCCCCTTCTTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAANANTACCCNTATCATCNNTGAATAAAAGGCCCCTGAAC---GANATGCTTCCANCANCCTTTAAGAC
510 520 530 530 540 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 710 720 730 740 750 760 ANGAATTCAGGAATTCCCCAGCCCCTCCTC
                                                                                                                                                                                                                                                               560 570 580 590 600 610 620 AAAGCCCCGTGTGGCAACTTCACTGA-GTGGATAGA
                                                                                                                                                                                                                                                                                         TTGATGGTATCACTGCCACNTTTCCACCCAGCTGGGCNCCCTTCCCCCATNTTTGTCANTGANCTGGAAGGC 370 380 430 410
                                                                                                                                                                                                                                                                                                                                                    630 640 650 660 670 680 690 GAAAACCCATGAAATTGACCCCCAAAATACATCCTGCGGA
                                                                                                                                                                                                     490 500 510 520 530 540 550 GACTCCTGCAACGGGTACTTGTGTGTCTTTCGGA
                              410 420 430 440 450 460 470 480 GUCTGCAGTGTTCTGCGCCGGCGGAAGACCAGAAG
340 350 360 370 380 400 TGGGGTCTGCTGCGTGAACGTGTGGTGTCTGAGGAN
                                                                                                                 Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-030-606-175 (1-1167)
US-09-020-747-11 Sequence 110, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Optimized Score = 401
Matches = 447
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGAACTCAAGAAGGTCTNNGAAAAACCACNCN
790 810 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 56
378
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial Score = Residue Identity = Gaps
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 1150 1160 x TAAGAGAAGCGCAAAAAA

THE H | HILL | CTCGAGCAGCTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACA 1340 1350 X 1360 1370 1380 1390 1400

1. US-09-030-606-175 (1-1167) US-08-904-809-38 Sequence 38, Application US/08904809 Initial Score = 55 Optimized Score = 204 Significance = 0.33
Residue Identity = 31% Matches = 235 Mismatches = 489
Gaps = 31 Conservative Substitutions = 0

| 550 | 660 | 670 | 680 | 690 | 700 | 710 | 720 | GGGGACCCATGAATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATATCTGTTCCCAGGGAACCCAGGGAATTTTCAGGAATATCTGTTCCCAGGGGAATATCTGTTCCCAGGGGAATATCTGTTCCCAGGGAATTTTAACCC-TTAAATCCCTCCGAAATTGAAGGAAAATTCNCCTAAGGCTNTTTGAAGG230 | 240 | 250 | 260 | 270 | 280 | 290

TGGGTCTGGTCGCCATTACTTTGCTACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGT 730 740 750 100 110 120 130 140 150 160 GITTCCAGAACTCCTACACCATCGGGCCTGGGCCTGCACAGGCCCGACCAAGAG---CCAGGGAGCC 170 180 190 200 210 230 230 AGATGGTGGAGGCCAGCCTCTTCCTTGCTCGCTAACGACCTCATGC CCGCGCTCTGCGGGGCCTCTGCGTGTTCTCCGTACGTGGTGGTGGTGGTGGTGGTCGAGGCCAGGG 540 540 540 
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650 670 680 960 970 980 1000 TCAGAGGTCCAAGCCCCCAGTCCCCAGACGTNCAGGTCCCAG TCCTCCNTCAGACGCAGGACCCCCCAGCCCNTCNTCCGTCAGACCCAGGGGTGCAGGCCCCAAAC -TTTCCT 800 810 820 830 840 850 860 GCCCTCOTCOTCAGACCCAGGCCCC Significance Mismatches GTINGALTIAAACCCCCTINANTINITIINACCCNNGNCINAANIATITNGNIICCGGIGI 300 340 350 Sequence 15, Application US/09071710 Optimized Score = 390 Matches = 466 Conservative Substitutions 22. US-09-030-606-175 US-09-071-710-15 940 950 CCCTCNTCCAGAG 25 Initial Score = Residue Identity = Gaps = GAAGCGCAAAAAAA 450 ccceeinceecce 720 x 1160 440 1010

1050 1060 1070 1080 1090 1110 CCACCTAGGANTICCCTGTACCAGTTGGTTTTTC 980 990 1000 1010 1020 1030 1040 CAACCCCTCGTCGAGGCCCAGAGGTNCAGGGCCCTCGTCCTCAGAGCCC--AGCGGTCCAATG TGTCTAATATTTGGGTAGGGTGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGAT 1480 1520 1530 1540 860 870 880 890 900 910 ---TCCAGCCCCCAGCCCTCCTTCAGACGCTCAG CAGGCATTTAAATTTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGG 1410 1420 1430 1440 1450 1460 1470 GTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATATC AGAAAACTICCAGCACAITGGGGIGGAGGGCCIGCTCACIGGGICCCAGCICCCGCICCTGIIAGCCCA 760 770 780 830 --TGCAGTAAGCTCTATGACCCGCT -----AGGGGTGCAGGCCCCCAACCCTCNTCCAGAGTCAGAGGTCCAAGCCCC--TCATCAAGTTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCT--380 390 400 410 GCTGCACTGCGTGAGGTGTCTGAGGANGTC----GGAG----

1, 15, 15, 15, 15, 15, 15, 15, 15, 15, 1	1120			<b>.</b>			, d	1556			24. 1	Init: , Resion Gaps	Ü
	1120 1130 1140 1150 x  ATTTTTGTCCCTTCCCCTAGATCAGAAATAAAGTNTAAGAGAAGCGCAAAAAA	TACTCTCTAGGACTGGGCTGATGAAGGCACTGC 1770 1780 1790 1800	23. US-09-030-606-175 (1-1167) US-09-525-397-15 Sequence 15, Application US/09525397	Initial Score = 55 Optimized Score = 390 Significance = 0.33 Residue Identity = 37% Matches = 466 Mismatches = 699 Gaps = 66 Conservative Substitutions = 0	x 10 20 GCGCAGCCCTGCGGCGCAC CCGCGCTCTGCGGGGTGTGTCTCCGTACGTGGGTGAGCCCACCAGGGCCAGGCAGCCAGGGCAGCCAGGGAGCCAGGGAGCCAGGGAGCCAGGGAGGCAGGGAGGCCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGCAGGGAGGA	30 40 50 60 70 80 90  TGTCATGGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCACACT	100	170	240 250 260 270 280 290 290 TCATCAAGATTGGAGATCGTGTCCGAGCATCAGCATTGCTTCGCA 11	300   310   320   330   340   350   360   370   360   370   370   360   370	380 390 400 410  GCTGCACTGCACGTGACGTGTCTCAGGANGTCTGCAGTAAGCTCTATGACCCGCT	440       450       460       470       480       490       500         GTACCACCCCAGCATGTTCTGCGCCGGGGGGGAGGCCAGAAGGACTCCTGCAACGGTGACTC       1   1   1   1   1   1   1   1   1   1	510 520 530 540 550 560 TGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTCTTTCGGAAAAGCCCCGTGTGGCC 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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US-09-841-894A-1 Sequence 15, Application US/09841894A
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RGGGCTGCCGGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCTGTGCT

RGGGCTGCCGGCCAGTTTCTGTTGCTGCCAAAGTAATGTGCTCTCTGCTGCCTGTGCT

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                                                 GTITCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCCGACCAAGAG---CCAGGGAGCCTGTTGAGGCCGACCAAGAG---CCAGGGAGCC
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                                                                     CAGGCATTTAAATATTTAATTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGG
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-TCCAGCCCTCCTCCNTCAGACGCAGGAGTCCAGACCCCCCAGCCCNTCNTCCGTCAG
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Mismatches
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US-09-071-710-16 Sequence 16, Application US/09071710
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Matches = 464
Conservative Substitutions
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TGGGGCTGCCGGGCTGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGGCTCTCTGCTGCCACCCTGTGCT 340 850 860 870 880 890 900 910	380 390 400 410 420 430 440  GCTGCACTGCGTGACGTGTCTGAGGANGTCTGCAGTAAGCTCTATGACCGGTGTACCACC	450 460  CAGCATGTTCTGCGCCGGCGCGAGGGCAAGACCAGAAGGACTCCTGCAACGGTGA	500         510         520         530         540         550         560           CTCTGGGGGGCCCTGTGTCTTTCGGAAAGCCCCGTGTGGC           I	570         580         600         610         620         630           CAACTTGGCGTGCCAGGTGTCACCAGCTCCAGNCC         1	40   650   660   670   680   690   700   710   AGTTAACTCTGGGGACTGGGAACCCATGACATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATAT	720 730 740 750 760 770 780  CTGTTCCCAGCCCTCCTCCTCAGGCCCAGGAGTCCAGGCCCCCCAGCCCTCCTCCTCCTCAAACCAAGGTA	790 800 810 820 830 840 850 CAGATCCCCAGCCCTCCTCCTCCTCAGACCCCAGCCCCCCAGCCCCTCNTCCNTCAGACCC	860 870 880 890 900 910  AGGAGTCCAGCCCCTCCTCCNTCAGAGGAGTCCAGACCCCCCCAGCCCNTCNTCCGTCA	920 930 940 950 950 970  GACCCAGGGGTGCAGGCCCCCCAACCCTCNTCCNTCAGAGTCAGAGTCCAAGCCCC	980 990 1000 1010 1020 1030 -CAACCCCTCGTTCCCCAGAGGTNCAGGTCCCAGCCCCTCCTCCTCAGACCCAGCGGTCCAAT	1050	CATTTTTGTCCCTTTCCCCTAGATCAGAATAAAGTNTAAGAGAGCGCAAAAAAA  CATTTTTTTTTTTCCCCTAGATCCAGAAATAAAGTNTAAGAGAGCGCAAAAAAA

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170 180 190 200 210 220 230 agategregaegecaececaeaegecaececaegecaececaegecaececaegecaececaegecaececaegecaececaegecaececaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecaegecae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.33
1770.
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    1760
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US-09-525-397-16 Sequence 16, Application US/09525397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Optimized Score = 393
Matches = 464
Conservative Substitutions
                                                                                                                             CTACTCTCTAGGACTGGGCTGATGAAGGCACTGC 1780 1790 1800
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378
67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial Score
Residue Identity
Gaps
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TGĞĞACCCATGAAATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATAT 640 AGTTAACTCTGGGGAC

GCCACCTAGANTNTCCCTGTACACAGTGCCCCTTGTGGCANGTTGACCCA--ACCTTACCAGTTGGTTTTT 1050 1630

CATTTTTGTCCCTTTCCCCTAGATCCAGAAATAAAGTNTAAGAGAAGCGCAAAAAAA CAGGTCTCAACGGCT

CTACTCTCTAGGACTGGGCTGATGAAGGCACTGC 1780 1790

27. US-09-030-606-175 (1-1167) US-09-841-894A-1 Sequence 16, Application US/09841894A

X 10 20 GCGCAGCCCTGGCAGGCGGCAC 0.33 Significance Mismatches Optimized Score = 393 Matches = 464 Conservative Substitutions 55 378 67 Initial Score = Residue Identity = Gaps =

GIGCCCTACCGCGGGGAACTCTTGCCTCGTNTCTGGCTGGGGTCTGCTGGCGAACGGCAGAATGCCTACCGT 330

----AGGGCAAGACCAGAAGGACTCCTGCAACGGTGA CAGCATGTTCTGCGCCGGCGG

CAACTIGGCGTGCCAGGTGTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGNCC 900

| 640 | 650 | 660 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710 | 710

260

AGGGGTGCAGGCCCCCAACCCTCNTCAGAGTCAGAGGTCCAAGCCCC---GACCC--

Thu May

28. US-09-030-606-175 (1-1167) US-08-850-713-16 Sequence 16, Application US/08850713 Initial Score = 55 Optimized Score = 392 Significance = 0.33 Residue Identity = 38% Matches = 472 Mismatches = 693 Gaps = 65 Conservative Substitutions = 0

| 850 | 870 | 880 | 890 | 900 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910

 ACTCTCTAGGACTGGGCTGATGAAGGCACTGC 1780

29. US-09-030-606-175 (1-1167) US-09-020-747-15 Sequence 153, Application US/09020747 us-09-030-606-175.re

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290 300 310 320 330 340 350 TCAGCATTGCTTCGCAGTGCCTGGCGGGGAACTCTTGCCTCGTNTCTGGCTGGGGGTCTGGCGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 370 380 390 400 410 420 GCAGABATGCTACGTGTCTGAGGANGTCTGCAGTAAGCTCTATG
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ACCCGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGGGGCAAGACCCAGAAGGACTCCTGCAACGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 240 250 260 X 270 280 ACCICAIGCICATCAAGIIGGACGAAICCGIGICCGAGICIGACACCAICCGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCAAACTATACTTCGCTCGN
                                                                                                                                                                                                                                                                                                              20 30 x 40 50 60 70 CGGCACTGGTCATGGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCGCAG
                                                                               ACAANACCCANGANAGGCCACTGGCCGTGGTGTCATGGCCT X 10 20 30 40
                                                                                                                                     150 160 170 180 190 210 GACCAAGAGCCAGAGCCAGAGACTATGGTGGAGGCCAGAGACTCTTG
                                                                                                                                                                                                                                                                  GCTCAGCAGGAGCACATCAATAAAGTCCAAAGTCTTGGACTTGGCCTTGGAGGAAGTCATCAACACC 110 150 150 140 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.31 \\ 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 245 Significance
Matches = 281 Mismatches
Conservative Substitutions
Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30. US-09-030-606-175 (1-1167)
US-08-806-596-23 Sequence 23, Application US/08806596
Optimized Score = 95
Matches = 99
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACACGGAGINAGGAATT 280 X
                                                                                                                                                                                                                                                                                                                                                                                                                               GIGGAAGCGCCGICCA
260
                                                                       GCGCAGCCCTGGCAGG
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TCTTGCTCGCTAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score Residue Identity
  Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370
ATGCCTACCG
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---GCCAAINTGTCNCCGTTTATT 210 220

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10 x 20 30 40 50 60 70 gegendecendedecenterations of accorded contractions of the second contractions of the second contraction of the second contra
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TGGGTGCTGTCCAGAACTCCTACACCATCGGGCTGGGCCTGCACAGTCTTGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1080 1090 1100 1110 1120 1130 1140 TGTGGCANGTTGACCCTAGATCCAGAAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 950 960 970 980 990 1000 cccaaccctcntccntcagagtccaa--gcccccaaccctcgttcccagaggtnca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTTCCNNCNNCTTCCACCATCTTCNTTACNGGGTCTCCNCGCCNTCTCNNNCACNCCTGGGACGCTNT
520 550 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720 730 740 750 760 770 780 TCCCAGCCCTCTCCTCAAACCAAGGTACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -cctcgccnnctncnngaaancgnanacgtcgggttgnnannancgctgtgggnnngcgtctgcnccgcg 440 450 450 460 470
                                                                                                                   580 590 600 610 620 630 640 TIGGCGIGCCAGGIGICTACAAATICACIGAGIGGATAGAGAAAACGICCAGNCCAGIT
                                                                                                                                                                                                                                    ATCGGGTTTNNNNTGACCGNGCNNCCCTCCCCCCNTCCATNA--CGANCCNCCCGCACCACCACANNNGCNCG 300 310 320 350 360
NTNCCAGCNTCNCCTNCCNACCCTACNTCTTCNNAGCTGTCNNACCCCTNGTNCGNACCCCCCNAGGTCGGG 230 240 250 250
                                                                                                                                                                                                                                                                                                                                                                CNCCCCGNNCTCTTCGCCNCCCTGTCTNTNCCCCTGTNGCCTGGCNCNGNACCGCATTGA----370 380 400 420 420
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Mismatches ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08904809
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Matches = 248
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31. US-09-030-606-175 (1-1167)
US-08-904-809-27 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1150 1160
GTNTAAGAGGGCCAAAAAA
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30%
3
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Residue Identity
Gaps
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us-09-030-606-175.re

Conservative Substitutions

	150	220 230 240 250 260 270 280  CTCGCTAACGACTCATCATCATTGGACGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGC	290 340 350 360 360 360 360 340 350 360 ATTGCTTCGCAGCGCGCGCGCGCGCGCAACGCCAGCAGCAGCTTCGCTTGCCTGCTGCCTGC

ATGCCTACCGTGCACTGCGTGAACGTGTCGGTGTGTCTGAGGANGTCTGCAGTAAGCTCTATGACCCG

CNGCCCCNNCCCCCNGNATTAAGGCCTCCNNTCTCCGGCCNC 780 810 x

870 880 CTCCTCCNTCAGACGCAGGA

75 (1-1167) Sequence 6, Application US/09071710 32. US-09-030-606-17 US-09-071-710-6

Optimized Score Matches Initial Score -Residue Identity -

6h0

670

640

CTTGGCCAAATACTCAGCGTAG NTCCNTCAGACCCAGGAGTCCAGCCCTCCTCCNTCAGACGCAGGAGTCCAGACCCCCCAGCCCNTCNTCCG 630 640 650 660 670 x 690 690 AGAAAACGTCCAGGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAAATACATCTGCGG CTTGGCCAAATACTCAGCGTAG 630 640 650 660 670 x 680 690 AGAAAACGTCCAGGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAAATACATCTGCGG 74 Significance 80 Mismatches Significance Mismatches 34. US-09-030-606-175 (1-1167) US-09-841-894A-6 Sequence 6, Application US/09841894A US-09-030-606-175 (1-1167) US-09-525-397-6 Sequence 6, Application US/09525397 Optimized Score = 74
Matches = 80
Conservative Substitutions Conservative Substitutions Optimized Score Matches CTGTGCTGCTGAGGTGCGTANTGCACAGGTGGGGGGCTG 160 170 180 x CTGTGCTGCTGAGGTGCGTANTGCACAGCTGGGGGCTG 160 170 180 X 39.8 39.8 9 52 398 9 TCAGACCCAGGGGTGC TCAGACCCAGGGGGTGC Initial Score Residue Identity Gaps Initial Score
Residue Identity = Gaps

920 TCAGACCCAGGGGTGC 35. US-09-030-606-175 (1-1167) US-09-020-747-39 Sequence 39, Application US/09020747 Initial Score = 52 Optimized Score = 234 Significance = 0.28
Residue Identity = 33% Matches = 250 Mismatches = 497
Gaps = 6 Conservative Substitutions = 0

| 890 | 900 | 910 | 920 | 930 | 940 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950 | 950

1030 x 1050 1060 1070 1080
AGCGGTCCAATGCCACCTAGANTNTCCCTGTACACAGTGCCCCTTGTGGCANGTTGACCC
| | | |
NAATCNCCANC 750

36. US-09-030-606-175 (1-1167) US-08-806-596-9 Sequence 9, Application US/08806596 Initial Score = 52 Optimized Score = 227 Significance = 0.28 Residue Identity = 36% Matches = 278 Mismatches = 455 Gaps = 34 Conservative Substitutions = 0

  | 520 | 530 | 540 | 550 | 560 | 570 | 580 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590 | 590

us-09-030-606-175.res

37. US-09-030-606-175 (1-1167) US-08-806-596-24 Sequence 24, Application US/08806596

Initial Score = 52 Optimized Score = 231 Significance Residue Identity = 28% Matches = 238 Mismatches Gaps = 7 Conservative Substitutions

0.28

 | Second | S

| 810 | 820 | 830 | 840 | 850 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870

880 X 890 900 910 920 930 AGACGCAGGAGTCCAGACCCCCAGGGGTGCAGGCCC | |

CGGAANGG 810 X 38. US-09-030-606-175 (1-1167) US-08-806-596-20 Sequence 20, Application US/08806596 Initial Score = 51 Optimized Score = 213 Significance = 0.26
Residue Identity = 29% Matches = 231 Mismatches = 523
Gaps = 19 Conservative Substitutions = 0

CCCAGGGGTGCAGGCCCCCAACCCCTCNTCAGAGTCAGAGGTCCAAGCCCCCCAACCCCTCGTTCCCCAA 850 860 870 880 890 900 910 TCAGACCCAGGCCCCTCCTCCNTCAGACGCAGGAGTCCAGACCCCCCAGCCCNTCNTCCGTCAGA 780 790 810 810 820 830 840 AAACCAAGGTACAGATCCCAGGCCCTCCTCATCCA ---GNTGAGNTNGGGTTTNCCCCCCCCCANGGCCCCTCTCG 550 560 560 NANAGTIGGGGTTIGGGGGGCTGGGGATTITINTITCCCCTTCTTCCCCCCCCCCCC----NGGGANAGA 590 640 650 GGTTNGNGTTTTGNTCNNCGGCCCCNCCNAAGANCTTTNCCGANTTNANTTAAATCCNTGCCTNGGCGAAGT 720 680 680 690 700 710 720 990 1000 1010 1020 1030 1040 1050 gacccagaggtuccagcccctcctcagaggtcccagccctcagacccagaggtccaatgccacctagantntccctgt ATTGTTTTTNGCCACGCCTGAATTAATTGGNTTCCGNTGTTTTCCNTTAAANAAGGNNANCCCCGGTTANT 310 320 350 350 350 630 640 650 660 670 680 690 ACCGICCAGNCCAGITAACICIGGGGACIGGGAACCCAIGAAAITGACCCCCAAAIACAICCIGCGGAANGA 420 430 440 450 460 470 480
TGCAGTAAGCTCTATGACCGGCTGTACCACCCCAGCATGTTCTGCGCCGGCGGAGGCCAAGACCAGAAGGAC AGTTNAACCCANTAINANC----TINAATNCCIGGAACCNGINGNITCCAAAAAINTTAACCCTTAANT 170 180 210 210 NAATCCCCCNNCCCCAATTATACCGANTTTTTTNGAATTGGGANCCCNCGGGAATTAACGGGGNNNNTCC 380 390 400 410 410 340 350 360 370 380 400 410 GGTCTGCTGCGTGCTGCTGCTGCTGCTGCTGCTGCTGGTGTCGTGTCTGAGGANGTC 0.26 175 (1-1167) 80 Sequence 20, Application US/08904809 Optimized Score Matches CCNTTGNAGGGNTAAANGGCCCCCTNNCGGG CCTCCNAGAAAAAANCTCCCAG------530 540 51 29% 19 39. US-09-030-606-1 US-08-904-809-2 Initial Score = Residue Identity = Gaps ACACAGTGC

```
CCCAGGGGTGCAGGCCCCCAACCCCTCNTCCATCAGAGTCAGAGGTCCAAGCCCCCAACCCCTCGTTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTNGNGTTTTGNTCNNCGGCCCCNCCNAAGANCTTTNCCGANTTNANTTAAATCCNTGCCTNGGCGAAGT 720 680 690 700 710 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990 1000 1010 1020 1030 1040 1050 GACCCAGAGGTCCAATGCCACCTAGANTNTCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGACCCAGGAGTCCAGCCCTCCTCCNTCAGACGCAGGAGTCCAGACCCCCCAGCCCNTCNTCCGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCCNAGAAAAAAACTCCCAG-----GNTGAGNNTNGGGTTTNCCCCCCCCCCANGGCCCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 570 580 590 600 610 620 GCCCCGTGTGGCCAACTTGGCGTGCCAGGTGTCTACACCTCTGCAAATTCACTGAGTGGATAGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGTTTTNGCCACGCCTGAATTAATTGGNTTCCGNTGTTTTCCNTTAAAANAAGGNNANCCCCGGTTANT 310 320 350 360 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCGTCCAGNCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCAAATACATCCTGCGGAANGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAATCCCCCNNCCCCAATTATACGANTTTTTTGGGANCCCNCGGGAATTAACGGGGNNNNTCC
380 430 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            490 500 510 520 530 540 550 TCCTGCAACGGGTACTTGCAGGGCCTTGTGTTTCGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 430 440 450 460 470 480
TGCAGTAAGCTCTATGACCCGCCGCCACCAGCATGTTCTGCGCCGGCGGAGGCCAAGGACCAGAAGGAC
TTTTTTTTTTTTTT OF THE X
                                                                                                                                                                                                  340 350 360 370 380 390 400 410 GGTCTGCTGCGTGCGTGCGTGTCTGAGGANGTC
                                                                                                                                                                                                                                                     AGTINAACCCANTAINANC----TINAAINCCIGGAAACCNGINGNITCCAAAAINTITAACCCITAANT
170 180 220 230
                                                                                                                                         AAAACCCCCTCCATTNAATGNAAACTTCCGAAATTGTCCAACCCCCTCNTCCAAATNNCCNTTTCCGGGNGG
                                                                                  270 320 330 310 320 .330 GACACCGGGGGAACTCTIGCCTCGTNTCTGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCNTTGNAGGGNTAAANGGCCCCCTNNCGGG
```

1060 ACACAGIGC

Conservative Substitutions

us-09-030-606-175.re

40. US-09-030-606-175 (1-1167) US-09-020-747-20 Sequence 20, Application US/09020747

Initial Score = 51 Optimized Score = 213 Significance = 0.26
Residue Identity = 29% Matches = 231 Mismatches = 523
Gaps = 19 Conservative Substitutions = 0

1060

41. US-09-030-606-175 (1-1167) US-09-020-747-26 Sequence 26, Application US/09020747

Us-Us-14/-zb sequence zb, Application Us/UsUzU4/

Initial Score = 51 Optimized Score = 250 Significance = 0.26
Residue Identity = 31% Matches = 261 Mismatches = 559
Gaps = 15 Conservative Substitutions = 0

```
970 980 990 1000 1010 1020 1030 AAGCCCCCCCCCTCCTCCTCCAGGGGTCCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regnical cititation of the property of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNCINGANATICCACINNCGCCTNCCNICNATCNGNAANACNAAANACINICINACCCNGGGGAIGGGNNCC 660 710 720
CCAGACCCCCCAGCCCCTCNTCCNTCAGACCCAGGAGTCCAGCCCCTCCTCCNTCAGACGCAGGAGTCCAGA
                                                                                                                                                                                                            GCCCCTNNTACTCNTCTCCCTCTNTINTCCTGNCNCACTTTTNACCCCNNNATTTCCCTTNATTGATCGGA 630 640 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900 910 920 930 940 950 960 ccccccagecccraaccctrontcagagtcagagtcc
```

## ; (1-1167) Sequence 170, Application US/09020747 75 42. US-09-030-606-1' US-09-020-747-1'

20 30 40 50 60 70 80 90 CACTGGTCATCGCATCCGCAGTGGTGCTGTCAGCCGCAC  $0.25 \\ 172$ Significance = Mismatches = Optimized Score = 90 Matches = 94 Conservative Substitutions Optimized Score Matches 50 348 4 Initial Score Residue Identity Gaps

ACCTGTGGGCTGTTATG

| 170 | 180 | 190 | 200 | 210 | 220 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 

## GCGTGAACGT

Significance Mismatches 175 (1-1167) 15 Sequence 155, Application US/09020747 Optimized Score = 107
Matches = 116
Conservative Substitutions 50 37% 6 43. US-09-030-606-1 US-09-020-747-1 Initial Score = Residue Identity = Gaps = =

190

CAGCCCCTCCTCCNTCAGACGCAGGAGTCCAGA--CCCCCCAGCCCNTCNTCCGTCAGACCCAGGGGTGCAG 650 660 670 680 690 700 710 TAACTCTGGGGAACCCATGAAATTGACCCCCAAATACATCCTGCGGAANGAATTCAGGAATATCTG 720 730 740 750 760 770 780 Trecence of the Trece of the Tree 790 800 810 820 830 840 850 ATCCCCAGCCCTCCTCCTCCTCAGACCCAGGACCCCCCCAGCCCTCNTCAGACCCAGGAGTC ACTGGAAATAATAAAAACCCACA CTTGGCGTGCCAGGTGTCTACACCAACCTCTGCAAATTCACTGAGTGGATAGAGAAAACCGTCCAGNCCAGT 910 930 940 950 960 970 980 960 eccecaaccetenteagagteagagtecaageceeaacceteg

## US-09-030-606-175 (1-1167) US-08-904-809-46 Sequence 46, Application US/08904809

 $\begin{array}{c} 0.25 \\ 413 \\ 0 \end{array}$ Significance Mismatches Conservative Substitutions Optimized Score Matches 50 29**%** 14 Initial Score Residue Identity Gaps

740 730

CTCAAACCAAGGGTACAGATCCCCAGCCCTCCTCAGACCCAGGAGTCCAGACCCCCCTCNT  us-09-030-606-175.res

ACATGT 590

45. US-09-030-606-175 (1-1167) US-09-020-747-19 Sequence 19, Application US/09020747 Initial Score = 50 Optimized Score = 219 Significance = 0.25
Residue Identity = 32% Matches = 240 Mismatches = 490
Gaps = 19 Conservative Substitutions = 0

46. US-09-030-606-175 (1-1167) US-08-904-809-40 Sequence 40, Application US/08904809 Initial Score = 50 Optimized Score = 243 Significance = 0.25
Residue Identity = 36% Matches = 278 Mismatches = 474
Gaps = 19 Conservative Substitutions = 0

290	550         560         570         580         600         610           TCTTTCGGAAAAGCCCCGTGCCAACTTCACTGAG           I I I I I I I I I I I I I I I I I I I
280	590 600 TCTACACCAACCTC'     GGCCTCCGCAGGA
270	550 560 570 580  CTTCGGAAAAGCCCCGTGTGGCCAACTTGGCGTGCCAGGTGT
260	570 STGGCCAACTTGG           SGCGTCGTCGCTG
250	560 AAAGCCCGTGT(               FAANCGCGGTGG( 310
240	550 TCTTTCGGAAP 

| 10 | 70 | 780 | 790 | 800 | 810 | 820 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 | 830 |

CTATCTGNACCCCNCNTTTGTCTCANTNT 730 740 750 X

1050 AGANTNT 47. US-09-030-606-175 (1-1167) US-09-020-747-8 Sequence 8, Application US/0902074 Initial Score = 50 Optimized Score = 256 Significance = 0.25 Residue Identity = 34% Matches = 286 Mismatches = 513 Gaps = 26 Conservative Substitutions = 0

8. US-09-030-606-175 (1-1167) US-08-806-596-36 Sequence 36, Application US/08806596 Initial Score = 50 Optimized Score = 256 Significance = 0.25
Residue Identity = 35% Matches = 508
Gaps = 36 Conservative Substitutions = 0

10 420 430 440 440 450 460 470 480 GTCTGCAGTAAGCTCTATGACGCGGAGGCAAGACCAGGAAG | || || || || TTGTGTTTTA----C'

TCCNTCAGACCCAGGAGTCCAGCCCTCCTCCTCCNTCAGACGCAGGAGTCCAGACCCCCCAGGCCCNTCNTCCGT 

CAGACCCAGGGGTGCAGGCCCCCCAACCCCTCNTCCNTCAGAGTCAGAGGTCCAAGGCCCCCCAACCCCTCGTTC

CTGTACACAG

us-09-030-606-175.res

US-09-030-606-175 (1-1167) US-09-020-747-36 Sequence 36, Application US/09020747

0.25 508 0 Significance Mismatches Optimized Score = 256
Matches = 302
Conservative Substitutions 358 358 36 Initial Score = Residue Identity = Gaps =

```
NGAACTCAAGAAGGTCTNNGAAAACCACNCN 790 810 X
                                                         .1060
CTGTACACAG
```

50. US-09-030-606-175 (1-1167) US-08-850-713-13 Sequence 13, Application US/08850713

Optimized Score = 98 Significance = Matches = 102 Mismatches = Conservative Substitutions = 49 378 3 Initial Score = Residue Identity = Gaps

| 850 | 860 | 870 | 880 | 890 | 900 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910

1060 TACACAGTG

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us-09-030-606-175-inv.res made by tport on Thu 1 May 103 15:05:56-PDT.
                                                                                                                                                                       ! initial comparison of US-09-030-606-175' (1-1167) with: 043.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Standard Deviation 15.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total Elapsed 00:00:01.00
                                                                                                                        Query sequence being compared:US-09-030-606-175' (1-1167)
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The scores below are sorted by initial score. Significance is calculated based on initial score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEARCH STATISTICS
                                                   se Comparison of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARAMETERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPU
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30
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Number of sequences searched:
Number of scores above cutoff:
                tcs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
              IntelliGeneti
                                               FastDB - Fast Pairw:
Release 5.4
                                                                                   Results file
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V O O A
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STDEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                  \circ \ \Box \ \circ \ \Box \ \Box \ \Box \ \circ \ \Box \ \circ
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A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Sig. Fr	Frame
7 4 Scandard deviations above mean 7 7 Sequence 173, Application 1265 97 *** 3 standard deviations above mean ***	° 0
US-08-904-809-9 Sequence 9, Application US 801	_
-/4/-II Sequence IIU, Application 34IU 90 399 3.9 -747-12 Segmence 120 Application 90 87 89 3.7	
. US-09-020-747-17 Sequence 175, Application 1167 82 384 3.3	0
**** 2 Standard deviations above mean **** 2 Standard deviations above mean **** 373 2.5	
. US-09-020-747-9 Sequence 9, Application US 801 63 239 2.1	
. US-09-020-747-16 Sequence 168, Application 273 62 95 2.0	_
0. US-09-020-747-17 Sequence 171, Application 1248 62 382 2.0	
1. US-09-071-710-8 Sequence 8, Application US 342 61 117 2.0	
z. Us-09-525-39/-8 sequence 8, Application Us	
4. US-09-071-710-16 Sequence 16, Application 2152 61 390 2.0	
-525-397-16 Sequence 16 -841-894A-1 Sequence 16	00
**** 1 standard deviation above mean ****	
7. US-08-904-809-65 Sequence 65, Application 377 60 121 1.9	
8. 03-020-747-03 Sequence 03, Application 377 60 121 1:3 9. US-08-904-809-47 Sequence 47, Application 774 60 260 1.9	
0. US-08-806-596-9 Sequence 9, Application US 801 58 239 1.8	
1. US-09-071-710-15 Sequence 15, Application 2143 57 391 1.7 2 US-09-525-397-15 Sequence 15 Application 2143 57 391 1.7	
3. US-09-841-894A-1 Sequence 15, Application 2143 57 391 1.7	
24. US-09-071-710-6 Sequence 6, Application US 195 56 71 1.69 25. US-09-525-397-6 Sequence 6, Application US 195 56 71 1.69	00
1, US-09-030-606-175' (1-1167) US-09-020-747-17 Sequence 173, Application US/09020747	
Initial Score = 97 Optimized Score = 386 Significance = 4.36 Residue Identity = 37% Matches = 444 Mismatches = 711 Gaps = 40 Conservative Substitutions = 0	910
X 10 20 TTTTTTGCGCTTCTTTANAC 	O NAC TGG
10 20 30 40 50 x 60 70	
30 40 50 60 70 80 90 TTTATTTCTGGATCTAGGGAAAGGGACAAAAATGAAAAACCAACTGGTAAGGTTGGGTCAACNTGCCACA	ACA         ACA
100 110 120 130 140 150 160  AGGGGCACTGTACAGGANANTCTAGGTGGCATTGGACCGCTGGGTCTGAGGCAGGAGGGCTGGGAC-	AC- ACA
017 007 0KT 00T 0/T 00T 0CT	
170	rgg 1 rcc
240 250 260 270 280 290 GGGCCTGCACCCCTGGGTCTGANGANGGCTGGGGGGGGTCTGGACTCCTGCGTCTGANGG	NGG

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90 840 850 850 860 AGTCCCCAGCCAGCCAGCCAGANACGAGGCAAGAGTTCCCCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTCCCTCAAACCAAGGGTACAGATCCCCAGCCCTCCTCCTCAGACCCAGGAGTCCAGACCCCCAGCCC 800 910 910 920 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGAGCAAGAGTCTGTTGTACTCTGGGTGCCGTACGGAGAGGCTGGCCTCCACCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGAAAACCGTCCAGGCCAGTTAACTCTGGGGACTGGGAACCCATGAAATTGACCCCCCAAATACATCCTGC 720 730 740 750 750 760 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 780 770 780 770 780 ACAGCGGGTCATAGAGCTTCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590 600 610 620 630 640 650 ACCTGGCACACTTGGCCACACGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTAAGTTGCAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTGCAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTATGACCCCTGTACCACCCAGCATGTTCTGCGCCGGCGGGGGCAAGACCAG 520 530 540 550 550
                                                                                                                                                                                                                                                                                                    460 470 480 490 500 510 2AGATATITGGGGGTCAATTTCATGGGTTCC
320 330 340 350 360 370 CTGGGTCTGANGGANGAGGGGCTGGGGGTCTGGACTCCTGGGTCTGAGGGAGGAG
                                                                                                                                                                                                                  ----AGTCGCGGGGCT
                                                                                                                                                                                            cGAACGGTGAGCTCACGGGTGTGTGTCTGCCCTCTTCAAGGAGGTCCTCTGCCC-370 380 410
                                                                                                                                          300 310
AGGAGGGCTGGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAGGGCTGGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGTCTGCAGTAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           720 730
ACATGCTGGGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCATGAGGTCGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       870
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                                                                                                                                               300
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930 940 950 960 970 980 990
TIGAIGAGCATGAGCTAGCGAGCAAGAGTCTGTTGTACTCTGGGTGCCGTACGGAGAGGCTGGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 810 820 830 840 850 860 ACGGTAGGCATTCTGCC-----GTTCGCCAGACCCCAGCCAGANACGAGGCAAGAGTTCCCCGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 590 | 600 | 610 | 620 | 630 | 640 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 | 650 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANGACGCGCTACACTNCTGGACCTCCCNCTCCACCACTTTCATGCGCTGTTCNTACCCGCGNATNTGTCCC ANGACGCGGCTACACTTCATGCGCTGTTCNTACCCGCGNATNTGTCCC 380 370 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         520 530 540 550 560 570 580 AGTCCCCAGAGGTTAGGAGGTTGGTGTAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 450 460 470 480 490 500 510 GRAGGGGCCCAGGATGTATTGGGGGTCAATTTCATGGGTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00 310 320 330 340 350 ...360 370
AGGAGGGGTGGACTCCTGGGTCTGANGGANGAAGGGGCTGGGGGGGTCTGGGGTCTGAGGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCCTTGATCCTCCCAGGCTG x 10. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GNANGTIGACCCAACCTTACCAGTIGGTTTTTCATTTTNG
1180 1190 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                     3.97
                                                                                                                                                                                                                                                                                                                                                                                                                                          Significance
Mismatches
                                                                                                                                                                                                       Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score
Matches
               TTTCCCTGNACACAGTGCCCCCTTGTG-
1150 1160 1170
                                                                                                                                                                                                                                                                                                                                                     US-09-030-606-175' (1-1167)
US-08-904-809-9 Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 338 24
                                                                                             1160 X
TGCCGCCTGCCAGGCTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               # H H
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial Score
Residue Identity
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Initial Score Residue Identity • Gaps	CCTGAGGGAGAGGGGCTGGGAACAGATATTCCTGAATTCNTTCCGCAGGATGTATTTGGGGGTCAATTTCA  CCTGAGGGAGAGGGGCTGGGAACAGATATTCCTGAATTCNTTCCGCAGGATGTATTTGGGGGTCAATTTCA
4. US-09-030-606-17 US-09-020-747-12	
CACCTTCTAG 1450	360 370 380 390 400 410 420 430 CTGAGGGAGGAGGAGGGGGCCTGGACTCCTGGG
1140 TTCCATGACCAGTGC 	300 310 320 330 340 350  ANGGAGGAGGGGCTGGGTCTGANGGANGANGAGGGCTGGGGGTCTGGACTCCTGGGT
70 3AAACA           1310	230 240 250 250 270 280 290 290 GANGAGGGGGTTGGGGGGGCTTGGGGGGGCTTGGGGGGGTCTGGGGGG
1000 CCACCATCTGGCTCC          ACACTATGATGAAGG 1230 1240	160 170 180 190 200 210 220 AGGAGGGCTGGGACCTCTGGGGACGAGGGGTTGGGGGCTTGGACCTCTGACTCTGANG
930 SATTGATGAGCATGA 1	100 110 120 130  AGGGGGCACTGTGTACAGGGANANTCTAGGTGGCATTGGACCGCTGGGTCTGAGGG
sgragge sgragge l scgccge 1100	30 40 50 60 70 80 90 TTTATTTCTGGATCTAGGGGACAAAAATGAAAAACCAACTGGTAAGGTTGGGTCAACNTGCCACA
GTTCACGCAGTGCAG 	X 10 20 TITITIGCGCTTCTTANAC TITITITGCGCTTCTTANAC
710 GCGCAGAACATGCTC 11 CAGCGCTGGGCCCCP 950 96	3. US-09-030-606-175' (1-1167) US-09-020-747-11 Sequence 110, Application US/09020747  Initial Score = 90 Optimized Score = 399 Significance = 3.90  Residue Identity = 38% Matches = 460 Mismatches = 698  Gaps = 49 Conservative Substitutions = 0
AGTGCCTCTTTGGCC	1150 1160 ACCAGTGCCGCCTGCCAGGGCTGCGC
GCCTGGGCTACCTCG	1070
TGGGTTCCCAGTCCC	1000 1010 1020 1030 1040 1050 1060  ACCATCTGGCTCCTTGGTCGGCCTCAAGACTGTGCAGGCCCGATGGTGTAGGAGTTCTGG
510	

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CAGCGCTGGGCCCCACCGAGCCAGCAGCGCTGTTGTCGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCC
950 950 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TOTAL | TOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000 1010 1020 1030 1040 1050 1060 CCACCATCTGGCTCTTGGTCGGCCTCAAG----ACTGTGCAGGCCCAGCCCGATGGTGTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              710 720 730 740 750 760 770 780 GCGCAGAACATGCTGGGGTGGTA-CAGGGGTCATAGAGCTTACTGCAGACNTCCTCAGACACCCACGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11070 1080 1090 1100 1110 1120 1130 GTTCTGGAAACAGTGTGCGCTGACACCACCACCACCAGGACGCCCGGAACAATTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5' (1-1167)
Sequence 120, Application US/09020747
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US-09-020-747-12 Se
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1450
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3.71

Significance Mismatches

Conservative Substitutions

Optimized Score Matches

87 978 0

						<u>-</u>				
 ∷_∷	AG		3 3 0 0 1 1 1 1 1 1 1	-cgcT 	210 CCTC      TCTC	GAC	.ccr 	ACTC    	ICAA   3CGG ·	CAGA
600 610 620 630 640 X 650 660 GCCAAGTIGGCCACACGGGGCTTTTCCGAAAGACACAAGGCCCTGCAAGTACCGTTGCAGATCAGGGGCCC	670 680 700 X CCCAGAGTCACCGTTCTGGTCTTGCCCTCCGCCGGCGCAGAACATGCTGGGGTGGTACAG	780 ACACG	S-09-030-606-175' (1-1167)  S-09-020-747-17 Sequence 175, Application US/09020747  ial Score = 82 Optimized Score = 384 Significance = 3.38  due Identity = 39% Matches = 456 Mismatches = 663  due Identity = 39% Matches = 663  10 20 30 40 50 60 70  THITTTGCGCTTCTTANACTTTATTCTGGATCTAGGGGAAAGGGAAAAAAAAAA	80 130 130 120 130 130 130 130 130 130 130 130 130 13	190 200 rggggaacgacggcrrgga	220 240 280  TGACTCTGANGGANGAGGGGTTGGGGCCTGCACCCCTGGGTCTGACGGANGANGGGCTGGGGGGTTGGAC	290         340         350           TCCTGCGTCTGA - NGGAGGGGCTGGACTCCTGGGTCTGANGGANGAGGGGCTGGGGGTCTGGACTCCT         1   1   1   1   1   1   1   1   1   1	350   370   380   400   410   420	430 440 450 460 470 480 490 CTGGGCCTGAGGAGGGGCTGGGAACAATTCCTGAATTCNTTCCGCAGGATGTATTTGGGGGTCAA	10   520   540   550   560   560   550   560   550   560   550   560
610 620 630 GGGGCTTTTCCGAAAGACACAAGGCC	. 690 700 SAGGAGTCCTTCTGGTCTTGCCCTCC [11111111111111111111111111111111	740 750 760 770 780 CGGGTCATAGTGCAGAGACACCGACGACGACAGACAT	(1-1167) Sequence 175 82 Optim 39% Match 40 Conse 20 TTANACTTTATT	90 100 110 GCCACAAGGGGGCACTGTGTAC. 	160 170 180 GGGCTGGGACCTGNACCTCTGGGTC 	230 240 250 AGGGGTTGGGGGCCTGCACCCCTGGC	300 310 320 GAGGAGGGCTGGACTCCTGGGTCTG 	0 GGGGCTGGGGATCTGTACCCTTGGT' 	430 440 450 460 CTGGGCCTGAGGAGGAGGGCTGGGAACAGATATTCCTG	520 530  GTCCCCAGAGTTAACTGGNCTGGAC
600 GCCAAGTIGGCCACACG	670 680 CCCAGAGTCACCGTTGCJ                 CCCAGAGTCACCGTTGCJ	740 750 CGGGTCATAGAGCTTAC	5. US-09-030-606-175' US-09-020-747-17 S Initial Score = Residue Identity = Gaps	80 AAGGTTGGGTCAACNTG             CTGCTCGGGCGTCCTGG 50	140 150 160 170  GGGTCTGAGGGAGGGGCCTGGGACCTGNA(	220 TGACTCTGANGGANGA           CGTACGCCACCAGAG 190	290 TCCTGCGTCTGA-NGG            GTCCGAGTCTGACACC 260 270	360 370 GGGTCTGAGGGAGGAG             NTCTGGCTGGGGTCTG	430 440 CTGGGCCTGAGGGAG(                   TGAGGANGTCTGCAG'	500 510 TTTCATGGGTTCCCA 

570 580 GGTTGGTGTAGACAC

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X 10
TTTTTTGCGCTTCTCTTANAC
                                                                                                                                                                                                                                              GAGCCAGATGGTGGAGCCTCTCCGTACGGCACCCAGAGTACAACAGACCTTGCTCGCTAACGACCT 100 110 120 130 140 X 150 160
                                                                    920 930 940 950 960 970 980 990
TCCAACTTGATGAGCATGAGGTCGTTAGCGAGCAAGAGTCTGTTGTACTGGGTGCCGTACGGAGGGCTG
                                                                                                                                                                                                                    650 660 670 680 690 -700 710 ACCCGTTGCAGAGTCACCGCCGCCGCGCGCG
                                            2.54
749
0
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                                                                                                                                                                                                                                                                                                                                                                                                          Significance
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                      ; (1-1167)
Sequence 174, Application US/09020747
                                                                                                                                                                                                        970
                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 373
Matches = 416
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
                                                                                                                                                                                                                                                                                                                                     1140 1150 1160 X
TTTTCCATGACCAGTGCCGCCTGCCAGGGCTGCGC
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348
36
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US-09-020-747-17 Se
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 | 820 | 830 | 840 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850

7. US-09-030-606-175' (1-1167) US-09-020-747-9 Sequence 9, Application US/09020747 Initial Score = 63 Optimized Score = 239 Significance = 2.15
Residue Identity = 33% Matches = 266 Mismatches = 514
Gaps = 24 Conservative Substitutions = 0

440 450 460 500 510 6GAGGGGCTGGGAATTTCATGGGGTTCCC 510 6GAGGGGCTGGGAATTTCATGGGTTCCC 6GAGGGTTCCC 6GAGGTTCCC 6GAGGTTCCC 6GAGGTTCCC 6GAGGTTCCC 6GAGGTTCCC 6GAGGTTCCC 6GAGGTTCATGGGGTTCAAGGACAAGGCCACAAGGTTCCAAGGTTCAAGGACAAGGCCACAAGGTTCCT 6 110 120 130 140 150 150 160

Thu May

US-09-030-606-175' (1-1167) US-09-020-747-13 Sequence 133, Application US/09020747

770 780 GACACCACCGACAC

	. 6	Res Gap	•										
390 400 410 420 430 440 450	800       810       850       860         ACGTAGGCATTCTGCCGTTCGCCAGCAGCAGCCAGCAGAGCAAGAGTTCCCCGCGGTA	870   880   900   910   920	930 940 950 960 970 980 990  TTGATGAGGAGGAGGAAGAGTCTGTTGTACTCTGGGTGCCGTACGGAGGCTGGCCTCC	1000         1010         1020         1030         1040         1050         1060           ACCATCTGGCTCTTGGTCGGCCTCAAGACTGTGTGTGTGT	0         1080         1100         1110         1120         x         1140           AAACAGTGTGCGGCTGACCACTGCGGATGCACCAGGACGACCAGAACAATTCGTTTTCCATG         1	1150 1160 ACCAGTGCCGCCTGCCAGGGCTGCGC	US-09-030-606-175' (1-1167) US-09-020-747-16 Sequence 168, Application US/09020747	Initial Score = 62 Optimized Score = 95 Significance = 2.08 Residue Identity = 35% Matches = 98 Mismatches = 175 Gaps = 1 Conservative Substitutions = 0	410 420 430 440 450 460 470 GGGCTGGGGCCTGGGAACAGATATTCCTGAATTCCGCA  ACTTCTAAGATTTCTAGAAGTG  ACTTCTAAGATTTCTAGAAGTG  X 10 20	480 490 500 510 520 530 540 550 GGATGTATTGGGGGTCAATTCATGGGTTCCCAGAGTTAACTGGNCTGGACGGTTTTCTCTATC	S60   570   580   600   610   620   CACTCAGTGAATTTGCAGAGGTTGGTGTAGACACCTGGCACGCCCAAGTTGGCCACGGGGCTTTTCCGAAA	630 640 650 660 670 680 690  GACACACAGGCCTGCAGTACCCGTTGCAGGGCCCCCCAGAGTCACCGTTGCAGGAGTCCTTCTGG	700 710 720 730 740 750 760  TCTTGCCCTCCGCCGCCAGAACATGCTGGGGTGCTACAGCGGGTCATAGAGCTTACTGCAGACNTCCTCA
	7		TT     TA(	н	1070 A 740		8. U	Init Resi Gaps		4			

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        720
        730

        CAGAGTCACGTTGCTTTGGTCTTGGCCTCCGCCGCCGCAGAACATGCTGGGTGGTACAGCG
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TTTTTTGCGCTTCTCTTANAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 470 480 490 500 x 510 520 AACAGATATTCCCGCAGGATGTATTTGGGGGTCAATTTCATGGGTTCCCAGAGT
                                                                                                                                                                                                                                                                                                                      ACAAGCCTTCACAAGTTTAACT
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score = 382 Significance = Matches = 419 Mismatches = Conservative Substitutions =
Optimized Score = 90 Significance = Matches = 103 Mismatches = Conservative Substitutions =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0. US-09-030-606-175' (1-1167)
US-09-020-747-17 Sequence 171, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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TGCCGTTCGCCAGCAGACC
Initial Score = Residue Identity = Reps = Residue Identity = Reps = Residue Identity = Re
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390 400 410 420 430 440 450 CTGTACCCTTGGTTTGAGGGGGGGGGGGGGGGGCCTGGACTCCTGGGCCTGAGGA-GGAGGGGCTGGGA - GGAGGGGCTGGGA - GGAGGGGCTGGGGA - GGAGGGCTGGGA - GGAGGGCTGGGA - GGAGGGCTGGGA - GGAGGGCTGGGA - GGAGGGCTGGGA - GGAGGGCTGGGA - GGAGGCTGGGA - GAGGAGGCTGGGAGGCTGGAAGACCAGAAGACCTGCAACGGTG - ABO 510 510 520 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCTGGGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTTGTGTTTCGGAAAAGCCCCGTGTGGCC 550 550 560 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCTCCTCAGACCCAGACCCCCAGCCCCTCCTCCTCAGACCCAGG
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                                                                                                                                                                                                                                                                                                                                                             600 610 620 630 640 650 660 GTTGGCACACGGGGCCCTCCAAGTACCCGTTGCAGATCAGGGGCCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCAAGAC----TGTGCAGGCCCAGCCCGATGGTAGGAGTTCTGGAAACAGTGTGCGGCTGACAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCAACCTTACCAGTTGGTTTTTTTTTTTTTTCCCTTTCCCCTAGATAT
                                                                                                                                                                                                                                                                                                                                   750 760 770 780 790 800 810 CATAGAGCTTACTGCAGCACTCAGACATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCTCATCAAGTTGGACGAATCCGTGTCCGAGTCT-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 890 900 ATGCTCCGGATGGTGTCA
                                                                                                                                                                                                                                                                                                                                    530 540
AACTGGNCTGGACGGT
GCTCGCTAACGACCTC 270 280
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GITTTCTCTATCCACTCAGTGAATTTGCAGAGGTTGGTGTAGACACCTGGCACGCC.AGTTGGCCACACGGG
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                                                                                                                                                                                                                                                                                                                                                                      TTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAA
170 180 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 480 490 500 510 520 .530 ATTCNTCGCAGGATGTATTTGATGGGTTCCCAGTCCCAGAGTTAACTGGACG
                                   CACTGCGGATGCACCAGGACGCCCGAGCAGAACAATTCGTTTTCCATGACCAGTGCCGCCTGCCAGGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \frac{2.02}{221}
                                                                                                                                                                             \frac{2.02}{221}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score - 117 Significance
Matches - 120 Mismatches
Conservative Substitutions
                                                                                                                                                                            117 Significance
120 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310
                                                        11. US-09-030-606-175' (1-1167)
US-09-071-710-8 Sequence 8, Application US/09071710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12. US-09-030-606-175' (1-1167)
US-09-525-397-8 Sequence 8, Application US/09525397
                                                                                                                                                                                                    Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                             440
1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score
Matches
                                                                                                                                                                             Optimized Score
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGCTGATCCANCCCCTCTTACTTTATCA 320 330
1150
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35%
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Residue Identity
Gaps
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Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTTTCCGA
                                                                                                                                                                                                                            180
                                                                                                                                                                                                   Gaps
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620 GCTTTTCCGA 13. US-09-030-606-175' (1-1167) US-09-841-894A-8 Sequence 8, Application US/09841894A

Initial Score = 61 Optimized Score = 117 Significance = 2.02 Residue Identity = 35% Matches = 120 Mismatches = 221 Gaps = 1 Conservative Substitutions = (  TTTGCTGATCCANCCCCTCTTACTTTATCA 320 330

620 GCTTTTCCGA 14. US-09-030-606-175' (1-1167) US-09-071-710-16 Sequence 16, Application US/09071710 Initial Score = 61 Optimized Score = 390 Significance = 2.02
Residue Identity = 37% Matches = 452 Mismatches = 707
Gaps = 40 Conservative Substitutions : = 0

 | 850 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860

1150 1160 X CCAGTGCCGCCTGCCGC

GTAGAAGGGAATCCATTGCTTTTCTGTGTTGTCTAATATTTGGGTAGGGTGGGGATCCCCAACA

ATC

15. US-09-030-606-175' (1-1167) US-09-525-397-16 Sequence 16, Application US/09525397 Initial Score = 61 Optimized Score = 390 Significance = 2. Residue Identity = 37% Matches = 7 Gaps = 452 Mismatches = 7 Gaps = 40 Conservative Substitutions =

160

 | 520 | 530 | 540 | 550 | 560 | 570 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580 | 580

| 800 | 810 | 820 | 830 | 840 | 850 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860

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CACACAAGA	1070 TTCTGGAAA            ATCAGGATG	1140 TTTCCATGA      TTTAACAAA	TCCCCAACA 1520
	1010	1080   1090   1100   1110   1120   1130   1140   1140   1140   1140   1140   1140   1140   1140   1140   1140   1140   1140   11410	1150 1160 X CCAGTGCCGCCTGCCAGGGCTGCGC 
	1040 1050 TTGTGCAGGCCCAGCCGATGG1	1120 CGCCCGAGCAC TTTAAATATTT	ATATTTGGGT
	1040 ACTGTGCAGG             TTTTTGCTGA 40 13	1090	TIGGTGTCTA 1490
CATATGAAAGT1	1030 GTCGGCCTCAAGACT(         CACAGCACTGTCTTT 1330 1340	1100 CCACTGCGGAT( 	X CGC   CTTTTCTGTG X 1480
 GGATTTGAACA	1020 3GCTCTTGGT( 1 CAGCCCA(	1090 CTGACAGCACC           CCTTCTGTTGC	1160 GCCAGGGCTGC 
 ACTCCTCCATGG 0 1250	1010 TCTGGCTCCCTG(                   CCAGGTCCCCTC)	1080 GTGTGCGGC             GCCTGTTGGTC 1390	1150 1160 X CCAGTGCCGCCTGCCAGGGCTGCGC 
 ACAC 1240	AT:     AC( 1310	CAC TGC 1380	CC

X 10 20 TTTTTTGCGCTTCTTANAC Significance Mismatches ' (1-1167) Sequence 16, Application US/09841894A Optimized Score = 390 Matches = 452 Conservative Substitutions 61 378 40 16. US-09-030-606-17 US-09-841-894A-1 Initial Score = Residue Identity = Gaps = =

ATC

TAGTGCCTTCCTGCT 600 61

GCTGGGAACAGATATTCCTGAATTCNTTCCGCAGGATGTATTTGGGGGGTCAATTTCATGGGTTCCCAGTCCC 

| 740 | 750 | 760 | 770 | 780 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790 | 790

900 840 . 850 860 860 860 860 cerageage against a cerageage agains TAACAGCTAGCTCCTAGTTGAGACACCCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGG 1100 1110 1120 1130 1140

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ATGAGCATGAGGTCGTTAGCGAGCAAGAGTCTGTTGTACTCTGGGTGCCGTACGGAGAGGCTGGCCTCCACC

ATC

US-09-030-606-175' (1-1167)

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80 90 100 110 120 130 140 AAGGTTGGGTCAACNTGCCACAAGGGGCACTGTTACAGGGANANTCTAGGTGGACTTGGACCGCTGGGTC
                                                                                             20 30 70 70 2TTANACTTTATTCTGGATCTAGGGGAAAAGGGACAAAAAATGAAAAAACCAACTGGT
                                                                                                                                                                                           90 100 110 120 130 140 IGCCACAAGGGGCACTGTAGGAGGGCATTGGACCGCTGGGTC
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                                                                                                                                ACAACAANAANTCCCTTCTTAGG X 10 20
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Sequence 65, Application US/08904809
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5 Sequence 65, Application US/09020747
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TTTTTTGCGCTTCTC
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US-09-020-747-6
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                           Initial Score
Residue Identity
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        660

        GCCAAGTTGGCACACGGGGCCTTTTCCGAAGGACCACGTTGCAGATCAGGGCCCC
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                                                                                                                                                                                                                    | 10 | 290 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 | 340 |
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                                                                                                                                                                                                                                                                                                                                                240 250 - 260 270 280 X 290 300 TTGGGGGGCCTGCACCCCTGGGTCTGANGGAGGAG
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Mismatches
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US-08-904-809-47 Sequence 47, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative Substitutions
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388
46
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Residue Identity =
Gaps
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ATCAGGGGCCCCCCAGAGTCACCGTTGCAGGAGTCCTTCTGGTCTTGCCCTCCGCCGCGCGCAACATGCTG 530 540 550 560 570 580 2TGGNCTGGACGGTTTCTCTATCCACTCAGTGAATTTGCAGAGGTTGGTGAACA 380 400 410 420 430 GGGCTGGGGATCTGTACCCTTGGTTTGAGGGAGGGGCTGGGGG---CCTGGACTCCTGGGCCTGAGGGA 10 450 460 470 480 490 500 510 GGAGGGGCTGGGAACAGATTCCTGAATTCCGCAGGATGTATTTGGGGGTCAATTTCATGGGTTCCC 320 340 350 360 370 370 360 370 300 370 370 370 370 370 ACGCCTTGATCCTCCCAGGCTG 1030 1040 1050 1060 1070 1080 1090 TCGGCCTCAAGACTGTGCGGCCCGAGCCCGATGTGTAGGAGTTCTGGAAACAGTGTGCGGCTGACAGCACC TCTGACTTGCCTGATTACTCCAGCATCTTGGAACAATCCCTGATTCCCCACTCCTTAGAG---GCAAGATAG 550 570 580 590 600 610 GUTGATGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCCAACTTGATGAGCATGAGGTCGTTAGCGAG TCTGCCGTTCGCCAGCAGACCCCAGCAGANACGAGGCAAGAGTTCCCCGCGGTAGGGCACTGCGAAGCAAT 1.82 5' (1-1167) Sequence 9, Application US/08806596 Optimized Score = 239
Matches = 266
Conservative Substitutions 20. US-09-030-606-17 US-08-806-596-9 300 310 AGGAGGGGCTGGACTC Initial Score \*\*
Residue Identity \*\*
Gaps

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170 180 190 200 210 220 ----GGACCTGNACCTCTGGGTCTGGGGGTTGGGGGCTTGGACTCTGACTCTGANGGANGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAGGCAGTGCTCCCACCTCCACCGCGCTCTGCGGGCCTCTGCTGATGTCTCCGTACGTGT
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TTTTTTGCGCTTCTCTTANAC
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AAACAGTGTGCGGCTGACCACCACCACGGACGACCAGAACAATTCGTTTTCCATG
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TTGATGAGCATGAGGTCGTTAGGGAGGAGGGAGGCTGGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGCTGAANTCCCCATNACCNNGNCTCNATGGANCCNTCCNTTTTAANNACNTT-..-CTNAACTTGGGAANA 610 620 620 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000 1010 1020 1030 1040 1050 1060 ACCATCTGGCTCCTGGCTCTTGGGTTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCCCTCGNCCNTNCCCCCNTTAATCCCNCTTGCNANGNNCNTCCCCCCNNTCCNCCNNNTNGGCNTNTNAN 670 680 690 700 710
                                                                                                                                                                                                                                                                                                                                                        870 880 900 910
GGGCACT------GCGAAGCAATGCTGGATGGTGGTCAGACTCGGACACGGATTCGTCCAAC
ANGACGCGGCTACACTNCTGGACCTCCCNCTCCACCACTTTCATGCGCTGTTCNTACCGGGGNATNTGTCCC 320 320 330 340. 350
                                                                   730 740 750 760 770 780 790 GGGTGGTACAGGGGTTACTGCAGACNTCCTCAGACACCACCGACACGTTCACGCAGTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 Significance
448 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCNAAAAAGGCCCNNNANCAATCTCCTNNCNCCTCANTTCGCCANCCCTCGAAATCGGCCNC
0 750 750 760 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' (1-1167)
Sequence 15, Application US/09071710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Optimized Score = 391
Matches = 448
Conservative Substitutions
                                                                                                                                                                                                              830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1150 1160 ACCAGTGCCGCCTGCCAGGGCTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score = Residue Identity = Gaps = -
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 230
 240
 250
 300

 GGTTGGGGGCCTGCACCCCTGGGTCTGANGGAGG
 270
 280
 300

 III | III

----TCATAGAGCTTACTGCAGACNTCCTCAGACACCACCGACACGTTCACGCAG TACAGCGGG-----

900 890 AGGCCACTGCGAAGC-Trecearcretaage

---CACAGCACTGTCTTTTGCTGATCCACCCCCTTTTATCAGGATGT 1320 1330 TCTGGCTCCCTGGCTCTTGGTCGGCCTCAAGACTGTGCAGGCCCCAGCCCGATGGTGTAGGAGTTCTGGAAAC CCAGGTCCCCTCAGCC 1310 1010

1150 1160 X CAGTGCCGCCTGCCGC

22. US-09-030-606-175' (1-1167) US-09-525-397-15 Sequence 15, Application US/09525397

1.76 Optimized Score = 391 Significance Matches = 448 Mismatches Conservative Substitutions 57 37 39 . . . Initial Score Residue Identity Gaps TTTTTTGCGCTTCTTANAC   410

210 190

 GCTGGGAACAGATATTCCTGAATTCNTTCCGCAGGATGTATTTGGGGGTCAATTTCATGGGTTCCAGTCCC

			;					
	660 TCAGGGGC         TGGGGCGT	730 TGGGGTGG        TGGACTTA	790 TTCACGCAG      CTCAGGGTT 1080	860 ccccccccT 	CCAACTTGA               	1000 CCTCCACCA           ACACAAGAA 1300	1070 rcrggaaac          rcaggargr	1140 FTCCATGAC
 	650 CCTTGCAGA       AGCTGGGGGC	720 CAGAACATGO      GGTTTCAGTC	780 CACCGACACG1       ATTACCCAGGC	850 SCAAGAGTTCCC        IAAACTCAGTC	920 CGGATTCGTC         GGAGTTTCT/	990 AGAGGCTGG(          AGGGGCAAC?	1060 IGTAGGAGT:     TACCTTTTA: 1360.	1130 CAATTCGTT: 
	0   600   610   620   630   640   650   660   660   ACGCCAAGTTGGCGGGGTTTTCGGAAAGACACAAGGCCCTGCAAGTACCGGTTGCAGATCAGGGGC   1   1   1   1   1   1   1   1   1	670   680   690   700   710   720   730	TACAGCGGGTCATAGAGCTTACTGCAGACNTCCTCAGACACCGCGACACGTTCACGCAGCTTCACGCAGGCTTCACGCAGGCAG	800   810   820   830   840   850   860	### ### ##############################	0         940         950         960         1000           TGAGCATGAGGAGGAGGAGGAGGCTGGCCTCCACCA           +	1010 1020 1030 1040 1050 1060 1070  TCTGGCTCCTGGCTCTTGGTCGGCCTCAGACTGTGCAGGCCCAGCCCGATGGTGTAGGAGTTCTGGAAAC	1080 1090 1100 1110 1120 1130 1140TGTGCGGCTGACACCCCACTGCGGATGCACCAGGACGCCGAGCAGAACAATTCGTTTTCCATGAC
 	630 ACAAGGCCC 	700 TCTTGCCCT	760 CAGACNTCC            CGGGACTCT	830 ACCCCAGCC? GGGTTTTTGC	900 .rggrgrcag       'raargragc	970 ACTCTGGGT       TGTAGGGGA	1040 TGCAGGCCCA           TGCTGATCCA	1110 ccaggacgcc 
   	620 CCGAAAGAC         CTGTGCTGC	690 GTCCTTCTGG 	750 ;AGCTTACTGC/ 	820 CGCCAGCAG       ACCTAGAGAA	890 ATGCTCCGGA        AGCTTCGTT	960 AGTCTĢTTGT     SAAAGTTATT	CTCAAGACTGT	1100 1110 TGCGGATGCACCAGGA 
	610 SGGGCTTTT       GCTGCCACC	680 CGTTGCAGGAG 	740 TCATAGA   111   GGCTCCATGCA	810 FTCTGCCGTT        FTGAGACACA	880 AATGCTG2       CTTAACCTGC	950 GCGAGCAAGA       TGAACATATC	20 1( FGGTCGGCC7       CACAGCA( 1320	90 13 SCACCCACTO
 ccagcrcccc 810	600 TTGGCCACAC       GTGGCTCTC1 880	670 AGAGTCACCC      rcrcrccccz	3         1030	800 CGGTAGGCA1    GCCTCCTAG1	0 GCGAAGC        TCTAAGCCCC	940 GAGGTCGTTAC       CCATGGGATT	010 1020 TCCCTGGCTCTTGC        CCCCTCAGCCC	0 1090 CGGCTGACAGC
l   ACTGGGTC( 800	ACGCCAAG' ACGCCAAG' 1   1   AAAGTAAT(	CCCCCA(	TACAGCGGG             TACAGGGAG	TGCAGC-AC	870 AGGCACTGCGAAGC-                 TTCCCATCTCTAAGCC	1230 TGAGCATG	1010 TCTGGCTCCC 	1080 AGTGTGCC
	Ω Ω					9		

23. US-09-030-606-175' (1-1167) US-09-841-894A-1 Sequence 15, Application US/09841894A

CIGICACIGCCIAIAIGGIGICIGCCGCAGGCCIGGGICIGGICGCCAITIACITIGCIACAGG-GIAGIA
660 670 680 690 700 710 720 ACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTGCTGCCGCCGCTGGCCGCCAGGTTTCTGTTGCTGCC TTTATTTCTGGATCTAGGGGAAAGGGACAAAAATGAAAAACCAACTGGTAAGGTTGGGTCAACNTGCCACA 450 460 470 480 490 500 510 GCTGGGAACAGATATTTGGGGGTCAATTTCATGGGTTCAGTCCCAGTCCC 520 530 530 580 CAGAGGACGGTTTTCTCTATCCACTCAGTGAATTTGCAGAGGTTGGTGTAGACACCTGGC 100 110 120 150 160 AGGGGCACTGTGTACAGGGANANTCTAGG----TGGCATTGGACCGCTGGGTCTGAGGGAGGGGGCTG-270 260

24. US-09-030-606-175' (1-1167) US-09-071-710-6 Sequence 6, Application US/09071710

GAGGAGG

Initial Score = 56 Optimized Score = 71 Significance = 1.69
Residue Identity = 38% Matches = 75 Mismatches = 118
Gaps = 2 Conservative Substitutions = 0

80 90 100 110 120 130 140 150
GGGTCAACNTGCCACAAGGGGGCACTGTGTACAGGGGANANTCTAGGTGGCATTGGACCGCTGGGTCTGAGGG

370 GAGGAGG 25. US-09-030-606-175' (1-1167) US-09-525-397-6 Sequence 6, Application US/09525397

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Thu May

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Initial Score
Residue Identity = Gaps
                                                                                                                    A 100% identical
                                                                                      The scores below
Significance is
                                                                                                                                                     Sequence Name
                                                                                                                                                                                                                            Name
                                  of
of
                                                                                                                                                                                                                            Sequence
                                 Number
Number
Number
                                                                         May 103 15:07:30-PDT
                                                                                                                                                  US-09-030-606-177 (1-1119) with:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          995
                                                                          tport on Thu 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         870
                                                                                                       Query sequence being compared:US-09-030-606-177 (1-1119)
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    penalty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K-tuple
Joining pena
Window size
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      622
                                                                          bγ
                                                                                                                                                  e initial comparison of
                                                                           made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARAMETERS
                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497
8
                                                                         030-606-177.res
                                                                                                                                                           0043.seq
2047.seq
8806596.seq
8850713.seq
8904809.seq
9020747.seq
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6
                                            ise
                                                                                                                                              Results of the File: 61300 File: 62520 File: US0881 File: US0891 File: US0990 File: US0900 File: US0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
> 0 <
0| |O IntelliGeneti
> 0 <
                                        FastDB – Fast Pairw
Release 5.4
                                                                         -60-sn
                                                                        Results file
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STDEV 0
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SECERS

Standard Deviation 56.61

Median 28

Scores

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Sig. Frame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCA(;AGTACAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.22
10.00
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                                                                                                                                                                                                                                                                                                                                                                           \frac{7.90}{7.88}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.65
                                                                                                                                                                                                                                                                                                                                                                                                                        6.47
6.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.01
                                                                                                                                                                                                    Opt.
Score
                                                                                                                                                                                                                                                                                                               Init. Opt.
Length Score Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1119 Significance
1119 Mismatches
                                                                                                                                                                                                                                                                                                                                                         **** 7 standard deviations above mean ****
17 Sequence 173, Application 1265 478
17 Sequence 175, Application 1167 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                    Init.
Length Score
                                                                                                                                                                                                                                                  1119
                                                                                                                                                                                                                                                                                                                                                                                                                                       378
Total Elapsed 00:00:01.00
                                                                                                                                                                                                                                                                                                                                                                      US-09-020-747-17 Sequence 173, Application 1265 4
.US-09-020-747-17 Sequence 175, Application 11667 4
.*** 6 standard deviations above mean US-09-020-747-17 Sequence 171, Application 1248 3
US-09-020-747-17 Sequence 174, Application 1459 3
.*** 2 standard deviations above mean US-08-904-809-45 Sequence 45, Application 234 1
US-09-020-747-45 Sequence 45, Application 234 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-020-747-10 Sequence 109, Application 1524
**** 0 standard deviation from mean *
                                                                                                                                                                        query sequence was found:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-030-606-177 (1-1119)
US-09-020-747-17 Sequence 177, Application US/09020747
                                                                                                                                                                                                                                                  1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Optimized Score = 1119
Matches = 1119
Conservative Substitutions
                                                                                                                                                                                                                                                 1. US-09-020-747-17 Sequence 177, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-904-809-23 Sequence 23, Application US-08-904-809-8 Sequence 8, Application US
                                                                                                                          , are sorted by initial score.
calculated based on initial s
                                          189792
410
410
                                                                                                                                                                      sequence to the
 CPU
00:00:00
                                                                                                                                                                                                                                                                                  The list of other best scores
                                            residues:
sequences searched:
scores above cutoff
                                                                                                                                                                                                                      Description
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| 810 | 820 | 840 | 850 | 860 | 871 | 872 | 873 | 874 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875 | 875

 2. US-09-030-606-177 (1-1119) US-09-020-747-17 Sequence 173, Application US/09020747

7.90 485 0 Significance Mismatches Substitutions 592 629 H 0 Score Optimized Scor Matches Conservative ( 478 548 30 1 1 1 Score Identity Initial Residue Gaps 140

3. US-09-030-606-177 (1-1119)
US-09-020-747-17 Sequence 175, Application US/09020747

Initial Score = 477 Optimized Score = 584 Significance = 7.88 Residue Identity = 55% Matches = 638 Mismatches = 472 Gaps = 39 Conservative Substitutions = 0

X

4. US-09-030-606-177 (1-1119) US-09-020-747-17 Sequence 171, Application US/09020747 Initial Score = 397 Optimized Score = 586 Significance = 6.47
Residue Identity = 54% Matches = 658 Mismatches = 458

Thu May

490

GACTATCATGATTACTGTGTTG-----ACTGTGCTGTCTATTGTACTAACCATGCCGATGTTTAGGTG 

| 840 | 850 | 860 | 870 | 880 | 890 | 900 | 800 | 890 | 900 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890

1070

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US/09020747 Application 7 (1-1119) Sequence 174, US-09-030-606-177 US-09-020-747-17 S 6.13 488 0 Significance Mismatches Optimized Score = 502 Matches = 543 Conservative Substitutions 378 51% 27 # H H Initial Score Residue Identity

Sequence 45, Application US/08904809

US-08-904-809-45

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				: "							· .	•
310	FTTC-               	CCGG	CTGTG       NAGGG	660 LATCC	730 CAGAG 11 11 CACAG 670	rgaaa   1     Saaat   4 0	CATTA .       AACTT	rgcrg             	1020 FTGGG	1090 AACAG 11 AAATC	ACAGT	
	440 TACCAT	.0 ATCAC	TTGAC 11 16 520	TTGGJ     GAGAJ	CCTAC	800 GTAGT	870 STTCCC 11 STTATA 810	10 3TGTA1 1   ACATA2	CTCCI  -  AAGCI  950	TAATA	GGAAZ	
	sgrrgi      CAGGC	51 CACTGC	580 CTGTC 	650 CCATCT	720 TTCTGA	CTGTJ	ATCGTC       ATCCTC	940 ATTAGT 11 SAATAAC	1010 GCTGC   NTTTC1	1080 GTGCTJ       HTTTATJ	CAGAGG	
	430 GGCAGG	O TGCTC	GATTA      CGTGA 510	CTCAA           	TAATT    AACAG	790 TTCTC     AACAC	860 TATGA:       GAAAA:   800	CTTCA       -TACC 87	TGCAT     TGATP 940	TTAGG       TGTG1	GTACC	
	CCCTG	50 ACTAC       ANTAA	570 ATCAT    TGCAA	640 TTGGCC' I ACAGGG( 580	710 CCCACA   1 GAGAGA 650	TTCAT GCAGA 20	GAATG      CAATA	930 CATTIC	1000 GCTCC     	1070 AACACA       TTCTGA	ACTGT	
	420 TCCCAA        CCAGAG	0 TGCTC 1 1 TCTGC	AGACT     ACTCC 500	GTCAC GTCAC GACAC	7 CATTC     AACTG	780 ACAAA:                 	850 ATGAT	O TCTAGCA      GGGAGCG	GTTGA   TGGAA 930	1 TTGTA 	GGTCA	
	4 GCTTT GACC 50	49 CTGGG     NGAGG	560 AAGTC I SAAGG	630 TTAGCG'        ACAGAGG	700 GTCAGC   11 GAGAGA 640	CCCTC     ACATG 10	TCACA   GACCT	920 GCAGGT   1   1   CACGG	990 GCCTA TTTGT	1060 GTGCAG   CCTAAA	rcaag	
	410 TGAGAA       GGGGGC	CCTCA 11 1 CCTGA	STCCG	rgaaa'     sggag	7 CAGTG	770 FACTC	840 GCAGG   1   1 GCGGT(	) CCAGG     ACTGT' 350	rcrcr   ATACC' 920	1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	STTGT	
	AGTGT	48( rgcato	550 PAGTT(	520 TAGGT(         SAAGGG( 560	690 CTGCTT( GACAAC)	SCTGG     ACAGAJ	SGTGT(       GAGG(	910 STACACO	980 FGGAT	SO FGGGA FGCAA(	CAGG( 1060	
	00 TTGGG1 1 CCCAG1 34	CTGC7 1   1   410	ACCA1	ATGTT	69 TTCC1	760 NGGATC     AGAA!	830 GGGTG(         GGGCC1	CTCAC	CTCC7         ATTC2	1050 TCAATGO 	X IAAAA III	
	400 GAGGCT 11 TCTGCC	476 PACGTC	540 CCAGC 11 11 CCGGC	10 TGCCG   AAGGG' 550	10   GAGAT             GAGAC   620	TTCAA    AAGAG	eccado 1 1	900 TCATG( 1   ACTAG	970 CAGGA     TATGC	0 'ATGGT   'TTAA?	AAAAA    GCATT	
	0 TGTGG 11 GGTCC 33	CAAGG       CGTGP 400	CT-AG         CTGCG	AACCA         	680 A-ATTG       ACAGGG	750 AGCTC       AAAGG	820 GAGCCT       CAACAG	ATCCC       ACCTG	CACCT       CGTTT 900	1040 GGCCCAT	1110 AAAAA CTTGT	
	390 CAGACT( 11 AAGGAG(	460 CAGTG 11111 CAGTG	530 ATCAA     ATGTT	00 GTACTI      CGACTO	CACTG    GACAC 610	CATAT   GAAGC 0	g rcred l Crrcc	890 TTTAAAT      CAAAAAC	960 GCAAC 111 GCATA	0 GAGAG   11 GTGAA 97	TGTTA 1 GTGGA 1040	
	380 390 400 410 420 430 440 ATCCAGTCCCAGACTGTGGGAGTGTGAGAAGCTTTCCCAACCCTGGCAGGGTTGTACCATTTC-	450       460       470       480       490       510         GGCAACTTCCAGTGCACGTCCTCCTCACTACTGCTCACTGCATCACCGGGGTGTCTCACTGCTCCTGCACCGGGGTGTCCGGGGTGTCCGGTGTTGTTGATGATGATGATGATGATGATGATGATGATG	20         530         560         570         580           AACACTGTGATCAACT - AGCCAGCACCATAGTTCTCCGAAGTCAGACTATCATGATTACTGTTGACTGTG         11	OTGICTATTGTACTAACCATGCCGATGTTAGGTGAAATTAGCGTCACTTGGCCTCAACCATCTTGGTATCC           CTGICTATTGTACTAACCATGCTTAGGTGAAATTAGCGTCACCTTGGTATCC           I<	670         680         690         700         710         720         730           AGTTATCCTCACTGA-ATTGAGATTTCCTGCTTCCACCATTCCCACATACTTCTGACCTACAGAGA         11	740         750         760         770         780         790         800           GTGAGGGATCATATCATGTCATTTCTCCTCTTGTAGTGAAA         1	810   820   830   840   850   860   870   850   860   870   860   870	880         900         910         920         930         940           CCCAAAGCCTTTAAATCCCTCAGTACACCAGGCAGGTCTAGCATTTCTTCATTTAGTGTATGCTG         CT         I	50         960         970         980         1000         1010         1020           TCCATTCATGCAACCTCCTGGATTCTCTGCCTAGTTGAGCTCCTGCATGCTGCTTGCT	1030         1040         1050         1090           GAGGTGAGGGGCCCATGGTTCAATGGGA-TCTGTGCAGTTGTAACACTTAGGTGCTTAATAACAG         1	1100 1110 x  AAGCTGTGATGTTAAAAAAAAAAAAAAAAAAAAAAAAA	4
	380 ATCCA( 11 GCCCT(	450 GGCAJ 1 ACCG:	520 AACAC      CACCC	590 CTGTC 1 GAGGC 530	AGTT2      AGATC 600	GTGA(      GAAT!	8 GGTG(   1 GCAG	880 CCCAA	950 TCCAT       TCGAT	GAGG! AGTT( 96(	AAGCT     CAAGT 1030	4 U 4 U

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2.46
                                                                                                                                                                                                                                                2.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.01
177 Significance
177 Mismatches
                                                                                                                                                                                                                                                177 Significance
177 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 Significance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-030-606-177 (1-1119)
US-09-020-747-10 Sequence 109, Application US/09020747
                                                                                                                                                                                                                           7 (1-1119)
Sequence 45, Application US/09020747
Optimized Score = 177
Matches = 177
Conservative Substitutions
                                                                                                                                                                                                                                                Optimized Score = 177
Matches = 177
Conservative Substitutions
                                                                                                                                                                                                450 460 470 480 490 GGCAACTTCCAGTGCAAGGACGTCCTGCTGCACTCACTGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  450 460 470 480 490 GGCAACTTCCAGTGCAAGGACGTCCTGCTGCATCCTCACTGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score
                                                                                                                                                                                                                                                170
758
0
170
75%
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                           US-09-030-606-177
US-09-020-747-45
 0 11 0
                                                                                                                                                                                                                                                 H II N
                                                                                                                                                                                                                                              Initial Score
Residue Identity =
Gaps
Score
Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Score
Initial
Residue
Gaps
```

510 520 540 550 570 6ATCACCCGGAACACTAGTCACCATAGTTCTCCGAAGTCAGACTATCATGA AGAACTITCIGCIGGCACGCGCTAGGGACAAGCGGGAGGGGCGTCTGAAGCGCACGICCCAGA
920 930 940 950 950 960 970 980 440 450 460 470 480 490 500 graccattegeractactectectect GIGIGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGIGACTTCCCAAGTATC 340 350 400 410 670 0 Mismatches = 433 Substitutions Matches Conservative TCGAGCATTTCCGGGT 850 100 CACACTGTTTCCAGAA Residue Identity Gaps

```
ACCCTNGINCGNACCCCCCNAGGICGGGITINNNNIGACCGNGCNNCCCCTCCCCCCNTCCAINA
ACCCTNGINCGNACCCCCCCNAGGICGGGITINNNNIGACCGNGCNNCCCCTCCCCCCTCCAINA
340
310
320
330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 40. 50 60 70 , 80 90 cg-gcactggtcatggaaaacgaattgttctgctcggggggtct--ggtgcatccgcagtggtgtcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X
GCGCACTCGCAGCCCTGGCAGG
                                                                                                                                                                                                                                       GCCCGGCTCCTCCCAGAACCAGTCCTGGGAGGATC---AAGGCCTGGATCCCGGGCC--GTTATCC 1350 1360 1370 1380 1410
                                                                                                                                                                                                                                                                                       -CCACTCACAGATTCCT
                                                                                                         ATGTATGATCGTGTTCCCATTACCCAAAGCCTTTAAATCCCTCATGCTCAGTACACCAGGGCAGGTCTAGCA
                                                                                                                             TITCITCATITAGIGIATGCTGTCCATTCATGCAACCACCTCAGGACTCCTGGAITCTCTGCCTAGTTGAGC
                     CACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCGCACCTGGTGGCCTTGTCTTGA
1210 1210 1220 1230 1240 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.65
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Significance
Mismatches
1190
                                                                                                                                                                                                                                                                                                                                                                                                                  9. US-09-030-606-177 (1-1119)
US-08-904-809-23 Sequence 23, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score = 188
Matches = 208
Conservative Substitutions
                                                                                                                                                                                                                                                                                     ATCTGGAGCTGCAGGTCCTTGGGGTAACAGGGACCACAGACCCCTCA
                                                                                                                                                                                                                                                                                                                              1170
     1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
298
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N 9 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Score Residue Identity Gaps
       1140
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GCCCTACCGCGGGGAACTCTTGCCTTTTCTGGCTGGGGGTCTGCTGGCGAACGATGCTGTGATTGCCATCC

Giggececcacicocitáacticotidatecaaaaacteacecerecacacacateaacaaaacece

740 GATCATA 10. US-09-030-606-177 (1-1119)
US-08-904-809-8 Sequence 8, Application US/08904809

Initial Score = 64 Optimized Score = 243 Significance = 0.58
Residue Identity = 34% Matches = 279 Mismatches = 512
Gaps = 28 Conservative Substitutions = 0

| 850 | 860 | 870 | 880 | 900 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910 | 910

11. US-09-030-606-177 (1-1119)
 US-09-020-747-8 Sequence 8, Application US/09020747

Initial Score = 64 Optimized Score = 243 Significance = 0.58
Residue Identity = 34% Matches = 279 Mismatches = 512
Gaps = 28 Conservative Substitutions = 0

					:			
	-		1 k* 1				,	
160	430 440 450 460 470 480 490 CCCTGGCAGGTTGTACCATTTCGGCAACTTCCAGTGCAAGGACGTCCTGCTGCTTCACTGGGT	530 540 550 560  STGATCAACTAGCCAGCACCATAGTTCTCCGAAGTCAG	630 AATTAGCGT   I GGATTTTGC	700 GTCAG       GCCCCATGT 440	770 TACTCCCCT         GCTCCTCCC 510	810         820         830         840           AGTGAAAGGTGCCCCTCTGGAGCCTCCCAGGGTGGGTGTGCAGGTCAC         111 <th>850         860         870         880         890         910           AATGATGATGTGTGTTCCCATTACCCAAAGCCTTTAAATCCCTCATGCTCAGGTACACCAGGGCAG         1   1   1   1   1   1   1   1   1   1  </th> <th>20 930 940 950 960 970 980  GTCTAGCATTTCTTCATTTAGTGTGTGTGTCCATTCATGCAACCACCTCAGGACTCCTGGATTCTCTGC</th>	850         860         870         880         890         910           AATGATGATGTGTGTTCCCATTACCCAAAGCCTTTAAATCCCTCATGCTCAGGTACACCAGGGCAG         1   1   1   1   1   1   1   1   1   1	20 930 940 950 960 970 980  GTCTAGCATTTCTTCATTTAGTGTGTGTGTCCATTCATGCAACCACCTCAGGACTCCTGGATTCTCTGC
150	480 TGCTGCATCC        AGCAGTGTAG	550 ATAGTTCTC       CANGTGGGC	620 TTTAGGTGAA     CCCACANGG	690 CTGCTTCAGT 	760 GGATGCTGG        NNATGCCCG	6GGTGGGTGTGG GGGTGGGTGTGG I I I TNCTANAACCGG	910 CTCAGTACAC	980 GACTCCTGGA:   
	470 GGACGTCCT          GGAGGTCCA	540 GCCAGCACCA1   1   1   1 TGCTGCCCC2	610 ATGCCGATG         AGGANAACG	0 GAGATTTCC           GCCTTGTCT 420	750 . GCTCTTCAA   1   1 ACAACCACA	0 GCCTCCCAGG      TCCACTNNT1	900 TCCCTCATG	970 -CACCTCAGG           NCNANCCCG
140	460 CCAGTGCAAG(       SCTGGAGCGG	530 SATCAACTAC         SCTCTGCCTT	600 TGTACTAACC   GCGGACTTCA 340	680 CACTGAATTG!         ACCTGGTTGGG	740 GGATCATATA   1.4   TGTTCTCCTT 480	820 CCCTCTGGAG(        AGNCCTGNAT( 550	890 GCCTTTAAA       GGTTAATNN 620	960 CATGCAAC-         CCCNCNNCN 690
130	450 CGCCAACTTO         CCTGAAAGTO	520 GAACACTGT	CTGTCTATTO	670 AGTTATCCTC         3GCCCCCC	AGAGGTGAGG AGAGGTGAGG           TTTNGGGAGT	810 AAAGGTGCG        SAAGGATCA	880 TTACCCAAA        TTCNTTNAG	950 CTGTCCATT         CCCNCCNNT 680
120	440 STACCATTTC         CGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	510 GCATCACCCGC         CCTGANCC	590 FTGACTGTGCT          NACACTGAGCC	660 TTGGTATCC!      CTGGGCCTCC	730 FGACCTACAGI 1111 5GACCACCTT	800 STTGTAGTG	870 STGTTCCCA        NTGTTCCTT	940 TTAGTGTATG       TTGTTANGCN
110	430 GGCAGGGTTC   11 CCGCGAGTAC	SI GCTCACTGC II I I GGCCGANGCC	580 TTACTGTG1       TGGGTCCAA	650 CTCAACCATC1 I TAAGGCTCATC	720 ATAATTTCT      CACTGTCNG	790 ATTTCTCCT(     CCCCANCCTC	860 TGTATGATCO J ACCCNCCTTI 590	930 TTCTTCATT'           TGTTNAAAT' 0
100	420	500         510         520         530         540         550         560           GCTCACTACTGCTCACTGCGAACACTGTGATCAACTAGCTAG	570         580         590         600         610         620         630           ACTATCATGATTACTGATGTTTAGGTGAAATTAGCGT         A         <	640         650         670         680         700           CACTTGGCCTCAACCATCTTGTATCCTCACTGAATTGAGATTTCCTGCTTCAGTGTCAG         1	710         720         730         740         750         760         770           CCATTCCCACATAATTTCTGACGACTACTACAAGGATGCTGGTACTCCCTT	780 790 800 810 820 830 840 CACAAATTCATTTCTCCTGTTGTAGTGAAAGGTGCGCCCTCTGGAGCCTCCCAGGGTGGGT	AATGATGAA? CGCNGTGGAA?	920 930 940 950 960 GTCTAGCATTCTTCATTTAGTGTATGCTGTCCATTCATGCAAC

0.57 Sequence 84, Application US/09020747 Optimized Score = 117
Matches = 123
Conservative Substitutions 12. US-09-030-606-177 (1-1119) US-09-020-747-84 Sequence 63 368 4

Initial Score = Residue Identity = Gaps =

ANNCG

CGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCTCATG 80 90 100 110 120 130 140 170 180 190 200 210 220 . 230 240 CAGATGGTGGAGGCCAGAGTACAACAGACCTTGCTCGCTAACGACCTCATG 810 820 840 850 870 870 AGGIGGCCCTCCCAGGGTGGGTGCAGGTCACAATGAATGTATGATCGTGTTCCCATT 670 680 690 700 710 720 730

TAICCTCACATGAATTCCTGCTTCAGTGTCAGCCATT----CCCACATAATTCTGACCTACAGA CCTGCCCACTCAGTGGCAACACCCGGGAGCTGTTTTGTCCTTTGTGGAGCCTCAGCAGTTCCCTCTTTCAGA ---AGCCACCATGCAGTGCTTCAGCTTCATTAAGACCA 130 140 880 890 900 910 920 930 940 ACCCAAAGCCTTTAAAATCCCTCATGCTCAGAGGCAGGTCTAGCATTTCTTCATTTAGTGTATGCT TCGATGGGGCATCCTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGTTTGTCAACGTGGGCT 230 240 250 250 260 250 270 30 40 50 60 70 80 90 ----TGGTCATGGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGCA 600 610 620 620 630 640 X 650 660 TCTATIGIACTAACCATGTCTTAGGTGAAATTAGCGTCACTTGGCCTCAACCATCTTGGTATCCAGT GTGAGAGCCAGGCGTCCCTGTG 320 330 X 340 350 360 370 380 ACCGCGGGGGAACTCTTGCCTCGTTGCTGGGGTCTGCTGCGAACGATGCTGTGATTGCCATCCAGT Significance = Mismatches = US-09-030-606-177 (1-1119) US-08-806-596-17 Sequence 17, Application US/08806596 Optimized Score = 155 Matches = 169 Conservative Substitutions ACTCACTGCCAAGAGCCCTGAACAGG----61 35% 16 AGCGTTNCCGCCTCATCCGG 370 380 Initial Score Residue Identity Gaps

ACTICCTCATCGCAGCGGGGGAGA         0       320       330       340       350       360       370         0       1030       1040       1050       1060       1070       1080       1090         GGAGGTGAGGGAGGGATCTGTGCAGTTGTAACACAGTTAATAAACAG       1   1   1   1   1   1   1   1   1   1	AAGCTGTGATGTTAAAAAAAAAAAAAAAAAAAAAAAAAA	US-09-030-606-177 (1-1119) US-08-904-809-17 Sequence 17, Application US/08904809  Tal Score = 61 Optimized Score = 155 Significance = 0.53  Gue Identity = 35% Matches = 169 Mismatches = 297  16 Conservative Substitutions = 0	600 610 620 630 640 x 650 660 TCTATIGTACTAACCATGCCGTGAAATTAGCGTCACTTGGCCTCAACCATTGGTATCCAGT	670 680 730  TATCCTCACTGAATTGAGATTTCCTGCTTCAGCCATTCCCACATAATTCTGACCTACAGA	740   750   760   780   790   800   GGTGAGGGATCATATAGCTCTTCAAGGATGCTGGTACTCCCTCACAAATTCATTC	### ### ##############################	### 890   900   910   920   930   94	950 960 970 980 990 1010 GTCCATTCATGCAACCACCTCAGGACTCCTGGATTCTCTGCCTAGCTGCATGCTGCCTCCTTGG	0         1030         1040         1050         1060           GGAGGTGAGGGAGCCCCATGGTTCAACACATTAGGTGCTTAATAAACAG           1	1100 x AAGCTGTGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ACTTCCTCATCGC 300 310 1020 1030 GGAGGTGAGGGAG 1 1 1 1 1 GCAAGTGTGCCCT	1100 AAGCTGTGATGT1	14. US-09-030-606 US-08-904-809 Initial Score Residue Identity Gaps	600 TCTATTGTACTAA	670 TATCCTCACTGA   1   1   1 CCTGCCCACTCA 30	740 GGTGAGGGATCAT 	810 AGGTGCGCCTC7   1	880 ACCCAAAGCCTTT	950 960 GTCCATTCATGCA           ACTTCCTCATCGC	1020 1030 GGAGGTGAGGGAC             GCAAGTGTGCCC7	1100 AAGCTGTGATGT1

880 890 900 910 920 930 940
ACCCAAAGCCTTTAAATCCCTCATGCTCAGTACACGGGCAGGTCTAGCATTCTTCATTTAGTGTATGCT GTGAGAGCCAGGCGTCCCTCTG
X 600 610 620 620 640 x 650 660 TCTATTGTACTAACCATCTTGGTGAAATTAGCGTCACTTGGCCTCAACCATCTTGGTATCCAGT ACTTCCTCATCGCAGCGGCGTTGTGTTTGCTCTTGGTTTCCTGGGCTGCTATGGTGTAGACGGAGA 300 310 320 330 340 350 350 Optimized Score - 155 Significance - Matches - 169 Mismatches - Conservative Substitutions -60 Optimized Score = 184 Significance = 39% Matches = 222 Mismatches = 31 Conservative Substitutions = 15. US-09-030-606-177 (1-1119) US-09-020-747-17 Sequence 17, Application US/09020747 16. US-09-030-606-177 (1-1119) US-08-904-809-69 Sequence 69, Application US/08904809 490 50 480 470 61 358 16 460 Initial Score
Residue Identity Initial Score Residue Identity Gaps 20 450 ATGGGT 520 ATGGGT 520 10

ACTAGICCAGIGGIGGAAII X 10 20 CGCAGCCCTGGCAGGCGGCACTGGTCATGGAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCGCAGT

ACCATTTCGGCAACTTCCAGGGCGACGTCCTGCTGCTCACTGGGTGCTCACTACTGCTCACTGCA ACCATTTCGGCAACTTCCAGGGACGTCCTGCTGCTCACTGGGTGCTCACTACTGCTCACTGCA ACCATATGTACCAAGTCCCAGCCCAACTTGGACACCTGTGCCTTCCATGAACAGCCAGAACTGCAGA----370 370 420 420 430

660 670 GGTATCCTCA

7 (1-1119) Sequence 69, Application US/09020747 17. US-09-030-606-177 US-09-020-747-69 S 184 Significance = 222 Mismatches = Conservative Substitutions Optimized Score Matches 99**%** 39**%** Initial Score -Residue Identity -

| 120 | 130 | 140 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150

GGTATCCAGTTATCCTCA

US-09-030-606-177 (1-1119) US-08-806-596-13 Sequence 13, Application US/08806596

Optimized Score = 150 Significance = Matches = 166 Mismatches = Conservative Substitutions = 60 C 33& 7 Initial Score Residue Identity Gaps

us-09-030-606-177.res

CATTACCCAAAGCCTTTAAATCCCTCATGCTCAGTACACCAGGGCAGGTCTAGCATTCTTCATTTAGTGTA | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940 | 940

TECTULCALLONDON TO THE TOTAL T 950 960 970 980 1010 1010 TGCTGTCCATGCATCCTCAGGACTCCTGGATTCTCTGCCTAGTTGAGCTCCTGCATGCTGCCTCC

1090 1100 1110 X ATAAACAGAAGCTGTGATGTTAAAAAAAAAAAA

GAANACTTCACTCA

US/08904809 Sequence 13, Application 3. 19. US-09-030-606-17 US-08-904-809-13

 $0.51\\317\\0$ E 0 H Significance Mismatches Optimized Score = 150
Matches = 166
Conservative Substitutions 60 33& 7 Initial Score
Residue Identity =
Gaps

960

GAANACTTCACTCA 530

20. US-09-030-606-177 (1-1119) US-09-020-747-13 Sequence 13, Application US/09020747

 $0.51 \\ 317$ Significance Mismatches Optimized Score = 150
Matches = 166
Conservative Substitutions 60 33% 7 0 0 0 Initial Score Residue Identity Gaps

CAGAGGTGAGGGGATCATATAGCTCTTCAAGGATGCTGGTACTCCCCTCACAAATTCATTTCTCCTGTTGTAG 770

| 10 | 810 | 820 | 830 | 840 | 850 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 |

CATTACCCAAAGCCTTTAAATCCCTCATGCTCAGTACACCAGGGCAGGTCTAGCATTTCTTTAGTGTA 920 910

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310 320 330 340 350 360 370 GCCCTACCGCGGGGGAACGCTGCTGCTGGCTGGGGGTCTGCTGCTGCTGTGTTGCCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 400 410 420 430 ----ACTGTGGGAGGCTGGGAGGTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 520 530 530 540 550 560 570 GCATCACCGGGAACACTGTGATTACTGT
                                                                                                                                                                                                                                              170 180 190 200 210 220 230 GGAGCCAGATGGTGGAGGCCTCTCCTTACGGCCAGACTACAACAACAGACCCTTGCTCGCTAACGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATTTCGGCAACTTCCAG----TGCAAGGACGTCCTGCTGCATCCTCACTGGGTGCTCACTACTGCTCACT
                                                                                                                                                                                                                      30 40 50 80 90 CGGCACTGGT---CATGGAAAACGAATTGTTCTGCTCGGGGCGTCCTGGTGCATCGCAGTGGTGCTGTCAG
                                                                                                                                                                            CCAGAGGCTGTGGGTGAGCCGCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGG 320 x 330 340
x 10 20 GCGCACCCTGGCAGG
                                                                                                          0.51
699
0
                                                                                                            373 Significance
419 Mismatches
                                                                                       Sequence 110, Application US/09020747
                                                                                                          Optimized Score = 373
Matches = 419
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460
                                                                            (1-1119)
                                                                                                             60
36%
30
                                                                            21. US-09-030-606-177
US-09-020-747-11 3
                                                                                                                                                                                       CCTGGCCCACTATGGT
280
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                                                                                                             Initial Score = Residue Identity =
                               GAANACTTCACTCA
530
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X 10 20 30 40 50 60 GCGCCACTGGCACTGGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTG
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660 670 680 690 700 710 720 TCTTGGTATCCAGTGTATTCCTGCTTCAGTGTCAGCCATTCCCACATAATTTCTG
                                                                                                                                                                                                                                                                                                         TCATIT -- AGIGIATGCIGICCATICATGCAACCACCICAGGACICCIGGAITCICIGCCIAGITGAGCICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCATGCTGCCTCCTTGGGGAGGTGAGGGAGGGCCCCATGGTTCAATGGGATCTGTGCAGTTGTAACACAT
                                                                                                         | 870 | 880 | 930 | 900 | 910 | 920 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 | 930 
                                                                                                                                                                                                                                                               ACCTACAGAGGTGAGGGAT---CATATAGCTCTTCAAGGATGCTGGTACTCCCCTCACAAATTCATTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.48
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Matches = 148 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-1119)
Sequence 160, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       960
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38%
119
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US-09-020-747-16 S
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```

23. US-09-030-606-177 (1-1119) US-08-904-809-72 Sequence 72, Application US/08904809 Initial Score = 57 Optimized Score = 163 Significance = 0.46
Residue Identity = 35% Matches = 188 Mismatches = 322
Gaps = 22 Conservative Substitutions = 0

  24. US-09-030-606-177 (1-1119) US-09-020-747-72 Sequence 72, Application US/09020747 Initial Score = 57 Optimized Score = 163 Significance = 0.46
Residue Identity = 35% Matches = 188 Mismatches = 322
Gaps = 22 Conservative Substitutions = 0

  25. US-09-030-606-177 (1-1119)

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GGNCTGTNCTGTCNNACTTTAATGGGCCNGACCGGCTAATCCCTCCCTCCCTTCCANTTCNNNNAACC 440 450 450 460 470 480 480 490 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCICITCAAGGAIGCIGGIACICCCCICACAAAITCAITICICCIGITGIAGIGAAAGIGCGCCCICIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCTCCCAGGGTGGGTGAGGTCACAATGATGATGTATGATCGTGTTCCCATTACCCAAAGCCTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 910 920 930 940 950 960 arccetcatgrangeragegagegageteragearteratecattcatgrange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 330 340 350 360 360 370 380 GCGGGGGAACTTGCCTTGCCTTGCTGGTCTGCTGGCGAACGATGCTGATTGCCATCCAGTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCNTNNCTNGGGGGGGUNGGTNNCTNCNCCTGNTNNCCCCNCTCNCNNTTNCCTCGTCGTCCNNCNNGC
                                                                                                                                                                                                                                                                               390 400 410 420 430 430 440 450 ASTRICGGAGGTTGTACCATTTCGGCAGTTCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                      50 470 480 490 500 510 520 530 GCAAGGACGTCCTGCTGCTCACTGCTCACTGCTGATCACTGGAACACTGTGATCA
                                                                               180 190 200 210 220 X 230 240 ATGGTGGAGGCCAGCCTCTCCGTACGCCAGAGTACAACAGACCCTTGCTCAACAACAGACCCTTGCTCATACTCATGCTC
                                                                                                         TCTGGGTGATGCCTCTTCCTC
                         241 Significance
288 Mismatches
Sequence 27, Application US/08806596
                         Optimized Score = 241
Matches = 288
Conservative Substitutions
US-08-806-596-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGCTTNCCNTCNTCTC 52
                     Initial Score = Residue Identity = Gaps =
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1110 AAAAAAAAAAAA

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030-606-223-inv.res made by tport on Thu 1 May 103 15:11:18-PDT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Standard Deviátion
12.69
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Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K-tuple
Joining penalty
Window size
                                                                                                                                                                                                  FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
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24
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410
410
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00:00:01.85
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24
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Number of sequences searched:
Number of scores above cutoff:
> 0 < 0 | 0 IntelliGenetics > 0 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
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The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

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Seq	  - 				-				717	1.	Initial Residue Gaps						

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Thu May

270 280 300 300 310 320 TTGTCAAGACAATGTAAGGAAA----TGCCCCAMAAYAWATTAAATTGACCATAATTACCAATA----TC TITITITITITITICAGIAATAATCAGAACAATATITATTITITATATITAAATTCATAGAAAAGTGCCT X 10 20 30 40 50 50 60 70 150 160 170 180 190 210 GAATAGCACACTCCTAAGACTTCCT--TTGGCAGCATTACTTT GGCCAINCCCCCNCTTTCGGGGTTTGGGNNTAGGTTGAATTTTTNNANGNCCCAAA 480 490 510 4. US-09-030-606-223' (1-383) US-09-020-747-10 Sequence 105, Application US/09020747 Optimized Score = 146
Matches = 189
Conservative Substitutions 220 230 230 TGA---TAAGAAGTCTCCAAATAAAATACAAAATTTTGGCACAGACAT-84 448 34 Initial Score = Residue Identity = Gaps = X 10 zu TTTTAAACATATAGCTTAATGG 240 250 260 270 280 290 300 ATACAAAATTTTGGCACAGACATGTCAAGACAATGTAAGGAAATGCCCCAMAAYAYWATTAAA CCCCCTCCATTGAATGAAACTTCCNAAATTGTCCAACCCCTCNNCCAAATNNCCATTTCCGGGGGGGG TAACCCATTATNAACTTAAATNCCTNGAAACCCNTGGNTTCCAAAAATTTTTAACCCTTAAATCCCTCGAA 200 210 200 250 250 ACCCNNGNCTNAANTATTTNGNTTCCGGTGTTTTCCTNTTAANCNTNGGTAACTCCCGNTAATGAANNNCCC 330 340 350 360 370 380 390 X 10 20 TTTTAAACATATAGCTTAATGG 100 110 120 130 140 160 CCCCCACCAAAGTTAAAATATAAATTGTCATTCCAAGAAAATCTTTTAGAATAGCACACTCCAAACAA 4.81 241 5.04 Significance Mismatches Significance Mismatches GGCCATNCCCCCNCTTTCGGGGTTTGGGNNTAGGTTGAATTTTTNNANGNCCCAAA 480 520 GGCCATNCCCCCNCTTCGGGGTTTGGGNNTAGGTTGAATTTTTNNANGNCCCAAA 480 500 500 510 (1-383) Sequence 38, Application US/09020747 ' (1-383) Sequence 38, Application US/08904809 Optimized Score = 126 Matches = 141 Conservative Substitutions Conservative Substitutions 85 35% 6 88 35& 6 2, US-09-030-606-223 US-08-904-809-38 3. US-09-030-606-22: US-09-020-747-38 Initial Score Residue Identity Gaps Initial Score = Residue Identity = Gaps = = 380 X TGTTTT 380 X TGTTTT

146 Significance 189 Mismatches

Thu May

us-09-030-606-223-inv.re

AGGAAGAAAAGGATTACGCATACTGTTCTT 440 440

Sequence 102, Application US/09020747 5. US-09-030-606-22: US-09-020-747-10

2.44 139 Significance 149 Mismatches Conservative Substitutions Optimized Score Matches 38.8 5 Initial Score Residue Identity Gaps X 10 TTTTAAACATATAGCTTAATGGTCAAAAC **TTTTTTTTTTTT**T

' (1-383) Sequence 83, Application US/09020747 6. US-09-030-606-22. US-09-020-747-83

2.44 242 0 Optimized Score = 124 Significance
Matches = 141 Mismatches
Conservative Substitutions 55 348 13 Initial Score
Residue Identity = Gaps

ACCGAATTGGGACCGCTGGCTTATAAGCGATCATGTCCTCCAGTATTACCTCAACGAGGAGGAGATCGAGT

TTTTAAACATATAGCTTAATGGTCAAAACAAGTGCAA

US-09-030-606-223' (1-383) US-08-904-809-39 Sequence 39, Application US/08904809

- 2.29 - 250 - 0 Significance Mismatches Optimized Score = 123 Matches = 133 Conservative Substitutions 33.8 6 Score Identity Initial Residue Gaps

TTTTAAACATATAGCTTAATGGTCAAAACAAGTGC

AATATAATTGTCATTCCAGGAAATCAAAATCTTTTA----GAATAGCACACTCCAAACAAGTGAKGGGAACA 160

210

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CTTGGGGGTTCCCTCCCCANACCAACCCCNCTGACAAAAGTGCCNGCCCTCAAATNATGTCCCGGCNNTCN
370 380 390 400 410 420 X 430
```

8. US-09-030-606-223' (1-383) US-09-020-747-39 Sequence 39, Application US/09020747 Initial Score = 53 Optimized Score = 123 Significance = 2. Residue Identity = 33% Matches = 133 Mismatches = 2 Gaps = 6 Conservative Substitutions =

 9. US-09-030-606-223' (1-383) US-08-806-596-25 Sequence 25, Application US/08806596 Initial Score = 53 Optimized Score = 114 Significance = 2.29
Residue Identity = 32% Matches = 130 Mismatches = 251
Gaps = 9 Conservative Substitutions = 0

 10. US-09-030-606-223' (1-383) US-09-020-747-13 Sequence 138, Application US/09020747 Initial Score = 51 Optimized Score = 119 Significance = 2.13
Residue Identity = 37% Matches = 137 Mismatches = 197
Gaps = 14 Conservative Substitutions = 0

 | 80 | 90 | 140 | 120 | 130 | 140 | 140 | 140 | 150 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |

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100 110 120 130 140 150 160 CCACCAAAGTTAAAAATTGTCATTCCAGGAAATCAAAAATTTTAGAATAGCACACTCCAAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGACACAGGCATTTAAATATTTAACTTA

1370 1380 1390 1400 1410 1420 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTCACCTGGTTTCCCATCTCTAAGCCCCTTAAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTT 1160 1170 1180 1200
                                                                                                                        X 10 20
TTTTAAACATATAGCTTAATGG
                                                                                                                                                                                                                             40 50 60 70 80 90
AAAAAGATTAATTTACAAAGTTGAAGACTGTGGTCCTATAACTNTTTCCC
                                                                                                                                                                                                                                                                   AGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTT 1160 1170 1180 1190 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                      170 180 190 200 210 220 230 AKGGGAACACTACTAAATTACTTTTGATAAGAAGTCTCCAAATAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAAATTTTGGCACAGACATTTTAATCTTGTCAAGACAATGTAAGGAAATGCCCCCAMAAYAYWATTAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 50 60 70 80 90 PAAAAGATTAATTTACAAGTATCAGAAGTGAAGACTGTGGTCCTATAACTNTTTCCC
                                                                                                                                                                        GGCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTC 1090 1100 1110 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTAAACATATAGCTTAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTCAGGGTTAACAGCTAGCTTGGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTC 1090 1100 1110 1150
                                                    2.13 \\ 233
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Mismatches
                                                     Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTG
 s' (1-383)
Sequence 16; Application US/09071710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09525397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 133
Matches = 144
Conservative Substitutions
                                                   Optimized Score = 133
Matches = 144
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23' (1-383)
                                                   51
368
9
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368
9
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TCAAAACAAGIGCAAT
| 1 | 1
                                                                                                                                                                                                                                                                                                                                                                             CTAGGATGAAACACTC
.230 1240
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TCAAAACAAGTGCAA1
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11. US-09-030-606-2:
US-09-071-710-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12. US-09-030-606-2:
US-09-525-397-1
                                                 Initial Score Residue Identity Gaps
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TTTT
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CAAAATTTTGGCACAGACATTTTAATCTTGTCAAGACAATGTAAGGAAATGCCCCAMAAYAYWATTAAATTG
                                                                                                                                                                                GCCTCAGGGTTAACAGCTACCTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTC . 1090 1100 1110 1120 1130 x 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTAAACATATAGCTTAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 180 230 230 200 210 220 230 AGGGGAACACTACTACATAAGAACTTCCTTAGAATTACATTAGCAATTACTTTTGATAAGAAGTCTCCAAATAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACCAAAGTTAAAATATAATTGTCATTCCAGGAAATCAAAATCTTTTAGAATAGCACACTCCAAACAAGTG
                                                                                                                                                               2.13
233
0
          Significance
Mismatches
                                                                                                                                                                                                                                                     GGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTG
0 X 1520 1530 1560
                                                                                                                                                                                                                                                                                          13. US-09-030-606-223' (1-383)
US-09-841-894A-1 Sequence 16, Application US/09841894A
                                                                                                                                                                                                                                                                                                                        Optimized Score = 133
Matches = 144
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                        51
368
9
                                                                                                                                                                                                                                                                                                                          0 8 0
                                                                                                                                                                                                                                                                                                                        Initial Score
Residue Identity
Gaps
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170 180 230 230 200 210 AKGGGAACACTACTAGATAATTCCTTAGACTTCCTTTGGCAGCATTACTTTTGATAAGAAGTCTCCAAATAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 260 270 280 290 310 CAAAATTTTGGCACAGACATTTTAATCTTGTCAAGACAATGTAAGGAAATGCCCCAMAAYAYWATTAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATAATTACCAATATCAG----TCCCTAAGATAATTTTTCTGAATGAAGAATTGTTTTTTTGTTTTGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X 10 20
TITTAAACATATAGCTTAATGGTCAAAACAAGT
                                                                                                                                                                                            TTTTAAACATATAGCTTAATGG
                                                                                                                                                                                                                          GGCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACCCTAGAGAGGGTTTTTGGGAGCTGAATAAACTC 1090 1100 1110 1120 1130 x 1140 1150
                                                                                                                                                                                                                                                                          30 40 50 60 70 80 90 TCAAAACAAGTGCAATAAAAGTTTACAAGAGTATCAGAAGTGAAGACTGTGGTCCTATAACTNTTTCCC
                                                                                                                                                                                                                                                                                                                       AGTCACCTGGTTTCCCATCTCAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTT 1160 1170 1180 1290 1200
                                                                                                                                                                                                                                                                                                                                                                                        CCACCAAAGTTAAAATATATATTGTCATTCCAGGAAATCAAAATCTTTTAGAATAGCACACTCCAAACAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.05
                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 137 Significance
Matches = 153 Mismatches
Conservative Substitutions
                                                                                                              Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTG
1530 1540 1550
AGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTG
1530 1540 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-383)
Sequence 53, Application US/08904809
                                                                                US/08850713
                                                                                                             Optimized Score = 133
Matches = 144
Conservative Substitutions
                                                                                Sequence 16, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
38%
9
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368
9
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GCAATAAAAGATTAATT
GGGATCCCCAACAATC
                                                              14. US-09-030-606-223
US-08-850-713-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGATCCCCAACAATC
1510 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15. US-09-030-606-22
US-08-904-809-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATAATTTAGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score Residue Identity = Gaps
                                                                                                          Initial Score Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 X
TTTT
```

```
AATGATTGGCAGGTCNGGTAAATNCCAAAACATATTCCAACTCAACACTTCTTTTCCNCGTANCTTGANTCT 370 370 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X 10 2.
TTTAAACATATAGCTTAATGGTCAAAACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 50 60 70 80 90 100 GCAATAAAAGATTTACAAGAGTATAAAGACTGTGGTCCTATAAACTNTTTCCCCCACCAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 120 130 140 170 AAAATATATAGAATAGCACACTCCAAACAAGTGAKGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGAAGTTTGGTATTTTTATGCAGCATTTTCTTTTTGCTTGATAACACTACAGAACCCTTAAGGACACTG 80 130 140
                                                                                                                                                                  cettaaaaaaaagretreaaarcrecacracraranaccecrecrercaegaraanacrecrtregaacaga
220 270 280 280
                                                                                                                                                                                                                                                                                                                             110 120 130 140 150 170 AAAATATATATATATATATTTCCAGGAAATCAAA----ATCTTTTAGAATAGCACACTCCAAACAAGTGAKGGGAA
                                                                                                                             250 260 270 280 290 300 310 ATTITGGCACAGACATTTAATTGTCAAGAAATGTAAGGAAATGCCCCAMAAYAYWATTAAATTGACC-
                                                                                                                                                                                                                                         ATTTTGGCACAGACATTTTAATCTTGTCAAGACAATGTAAGGAAATGCCCCAMAAXAXWATTAAATTGACC
                                                                                                                                                                                                                                                                                             2.05
230
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 Significance
153 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-030-606-223'.(1-383)
US-09-020-747-53 Sequence 53, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Optimized Score = 137
Matches = 153
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                             GTGTATTCCAGGANCAGGCGGATGGAATGGGCCAGCCCNCGGATGTTCC
440 450 460 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388
388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial Score
Residue Identity
Gaps
```

```
GTGTATTCCAGGANCAGGCGGATGGAATGGGCCAGCCCNCGGATGTTCC 440 440 450 460
                           450
```

US/09020747 23' (1-383) 5 Sequence 25, Application 17. US-09-030-606-2: US-09-020-747-2:

2.05 Significance Mismatches Optimized Score = 114
Matches = 130
Conservative Substitutions Initial Score = Residue Identity =

X 10 20 TTTTAAACATATAGCTTAATGG CAAGATAGTTAAGTGGGATCGAGACATGTAAGCAGNCNNCATGGAAGTTTGAAGATGCCGCATTTGGATTGG 340 350 x 390 400

cccccrracc 770 x 380 X TTTGTTT

3' (1-383) Sequence 10, Application US/09071710 18, US-09-030-606-2; US-09-071-710-1

 $\frac{1.97}{178}$ 98 Significance 110 Mismatches Conservative Substitutions Optimized Score Matches 49 368 9 Initial Score -Residue Identity -

| 120 | 130 | 140 | 150 | 150 | 140 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150

370 380 TGTTTTTTTGTTTGTTTTT

US-09-030-606-223' (1-383) US-09-525-397-10 Sequence 10, Application US/09525397

 $\frac{1.97}{178}$ Significance Mismatches Optimized Score = 98 Matches = 110 Conservative Substitutions 49 368 9 4 6 9 Score Identity Initial S Residue I Gaps

CTCTTACCTTTATCAGGATGTGGCCT X 10 

20. US-09-030-606-223' (1-383) US-09-841-894A-1 Sequence 10, Application US/09841894A

1.97 178 0 Significance Mismatches Optimized Score = 98
Matches = 110
Conservative Substitutions 49 36<del>8</del> 9 11 11 11 Initial Score = Residue Identity = Gaps = E

| 80 | 90 | 100 | 110 | 120 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 150 | 140 | 150 | 140 | 150 | 140 | 150 | 140 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 |

٠.

370 380 TGTTTTTTTGTTTGTTTT us-09-030-606-223.res

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us-09-030-606-223.res made by tport on Thu 1 May 103 15:10:17-PDT.
                                                                                                                              : initial comparison of US-09-030-606-223 (1-383) with: 43.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Standard Deviation 12.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total Elapsed 00:00:00:00
                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                     g compared:US-09-030-606-223 (1-383)
searched:
ove cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEARCH STATISTICS
                                      ise Comparison of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Median
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARAMETERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPU
00:00:00.95
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0.33
                                                                                                                                                                                    020747.seq
841894A.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mean
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                    25
           IntelliGenetics
                                                                                                                           Results of the File: 613004; File: 625204; File: USO8880; File: USO885; File: USO890; File: USO9021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                                          Query sequence being
Number of sequences:
Number of scores abor
                                     FastDB - Fast Pairwi
Release 5.4
                                                                Results file
                                                                                                                                                                                                                                                                             10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scores:
100-
                                                                                                                                                                                                                                                                                                                                                                                                                   SCORE
                                                                                                                                                                                                                                                                                                                          SECRESSES
                                                                                                                                                                                                                                   Z D Z M E K
                                                                                                                                                                                                                                                                                              OE
```

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

-030-606-223.res

60-sn

ATAGGACCACAGTCTTCACTTCTGATACTTGTAAATTAATCTTTTATTGCACTTGTTTTGACCATTAAGCTA ACCAGTTAAATATCCAAAATTAAAGGAACATTTTTAGCCTGGGTATAATTAGCTAAATTCACTTTACAAG 460 510 520

380 X TATGTTTAAAA

Sequence 116, Application US/09020747 2. US-09-030-606-223 US-09-020-747-11

3.97 171 0 Significance Mismatches Conservative Substitutions Optimized Matches 71 388 2 Initial Score Residue Identity Gaps

TCAATTTAATWRTRTTKTGGGGCATTTCCTTACATTGTCTTGACAAGATTAAAATGTCTGTGCCAAAATTTT 

TCACTTGTTTGGAGTGTGCTATTCTAAAAGATTTTGATTTCCTGGAATGACAATTATATTTTAACTTTTGGTG 

GACCACAGTCTTCACTTCTGATACTTGTAAA GGGGAAANAGTTATAG

(1-383) Sequence 93, Application US/09020747 3. US-09-030-606-223 US-09-020-747-93

125 Significance 147 Mismatches Optimized Score = 125 Matches = 147 Conservative Substitutions Initial Score = Residue Identity = Gaps

110

TTGTATTTTATTTGGAGACTTCTTATCAAA - - - - AGTAATGCTGCCAAAGGAAGTCTAAGGAATTAGTAGT 9.

240

210

TGTTTTGACCATTAAGCTATATGTTTAAAA TCIGGAATAATATATAAA
TCIGGAAATAAATATATAAA 3 (1-383) Sequence 58, Application US/08904809 US-09-030-606-223 US-08-904-809-58 Optimized Score = 81 Significance Matches = 81 Mismatches. Conservative Substitutions 62 40% 0 Initial Score Residue Identity Gaps

ACAGGGATATAGGTTTNAAGTTATTGTNATTGTAAAATACAT
X 10 20 30 40 <u>AAAACAAACAAACAAAAAAAAACAATTCTTCATTCAGAAAAATTATCTTAGGGACTGATATTGGAATATTGG</u>

GTATTTTATTTGGAGACTTCTTATCAAAAGTAATGCTGCCAAAGGAAGTCTAAGGAATTAGTAGTGTTCCCM

TCTAAGTTTGGT 190 x

(1-383) Sequence 58, Application US/09020747

Optimized Score = 81
Matches = 81
Conservative Substitutions Optimized Score Matches 62 40% 0 Initial Score Residue Identity Gaps

110

ATTATGGTCAATTTAATWRTRTTKTGGGGCATTTCCTTACATTGTCTTGACAAGATTAAAATGT-CTGTGCC

us-09-030-606-223.res

180	H	<u>:</u>	9.06 242 00	20 ACAAAAAAAC	TATATGTTTTC 160	90 RTRTTKTGGGG   1 CCAGCAAGCAT 230	160 GGAGACTTCTT          AAAGCTGTCAA	230 GAGTGTGCTAT          CAGTTTGCCTT	0 310 TATAGGACCAC       GTANGAGGTTC 440	380 ATATGTTTAAA               AAGGCTGTAAA 510	
170	220 230 240 250 260 270 TCACTIGITIGGAGIGIGCTATICIAAAAGAITITGAITITCCTGGAAIGACAAITAITITI 1	147	Significance Mismatches	X 10 20 AAAACAAACAAAAAAAAAA	CACACCATTAATAATGGTAAGATTGGTTTATGTGGTAGTGGTATTTTGGCACCCTTATATGTTTTTC 100 110 120 150 160	30 40 50 60 70 80 90  AATTCTTCATTCAGAAAAATTATCTTAGGGACTGATATTGGTAATTATGGTCAATTTAATWRTRTTKTGGGG	100 110 120 130 140 150 160  CATTICCTTACATTGACAAGATTAAAATGTCTGTGCCAAAATTTTGTATTTTGGAGACTTCTT	170         180         200         210         230           ATCAAAAGTAATGGAAGTCTAAGGAATTAGTAGTGTTCCCMTCACTTGTTTGGAGTGTGCTAT	40         250         260         310         310           TCTABABGATTTTCCTGGAATGACAATTATATTTTAACTTTGGTGGGGGAANAGTTATAGGACCAC	370 ACCATTAAGCT 	
160	260 FTCCTGGAATGA	Application US/09020747	ore = 132 = 137 Substitutions		TTAGTGGTATTTT 130	70 rGGTAATTATGC           AGTGAGTTTGAA	140 FGCCAAAATTTTC         CAATATGTC	TAGTGTTCCCN	280 FTAACTTTGGTC 	350 360 TGCACTTGTTTTG/   11 AAAAAAAAATTCA( 490	
150	250 AGATTTGAT1	Applicatio	ed Sco ative		TTATGTGATTT1 120	60 3GGACTGATAT1          1TAACTTAAAA	100 110 120 130  CATTTCCTTACATTGTCTTGACAAGATTAAAATGTCTGT	200 TAAGGAATTAC 	270 ACAATTATATTT 	340 35 AATCTTTTATTC 	
140	240 GCTATTCTAAA	(1-383) Sequence 71,	60 Optimiz 34% Matches 4 Conserv		TAAGATTGGT1 110	40 50 AAATTATCTTAGG           ATATTATTTCCA1	120 TTGACAAGATT        TTGTCATCTTT	190 CAAAGGAAGTC 	260 TCCTGGAATGA         ACTCTTAGAGA	330 .CTTGTAAATT!             TTTTAAAAAGT	
130	230 GTTTGAGTGT      TTTGGT X	US-09-030-606-223 US-09-020-747-71 S	Score Identity =	·	ATTAATAATGG 100	30 40 TTCATTCAGAAAAA 	110 CTTACATTGTC       1 TAATAAAGGT	180 AGTAATGCTGC I GTGACCCTACT 10	250 AGATTTTGATT     TATCAAATATA 390	320 CACTTCTGATA          CAATTTTGTAT	x a   ATGAAGAATTCTGCC 20 530
120	220 2 TCACTTGTTTGG 1         1 TCTAAGTTTGGT	6. US-09-0 US-09-0	Initial Sc Residue Id Gaps		CACACC	AATTCT 	100 CATTICC	170 ATCAAA    ATAGGT	240 TCTAAA     GAAAAA	AGTCTT       CCTCCT 450	X A   ATGAAG 520

130

110

100

80

70

2.73 199 0

11 11

Significance Mismatches

Optimized Score = 136 Matches = 152 Conservative Substitutions

56 418 9

Initial Score Residue Identity Gaps

(1-383) Sequence 130, Application US/09020747

7. US-09-030-606-223 US-09-020-747-13

GAGGGAACTTTTGGCCTTTTTCCTTTTTCTGTAGGCCGCCTTAAGCTTTCTAAATTTGGAACATCTAAG 150 150 170 180 190 200 210 caagctgaanggaaaaagggggttcgcaaaatcactcgggggaanggaaaggttgctttgttaatcatgccc 220 250 260 260 280 280 .70 180 190 200 210 220 230 CA----AAAGTAATGCTGCCAAAGGAAGTTAGTAGTAGTGTTCCCMTCACTTGTTTGGAGTGTGC 240 250 260 270 280 290 300 TATTCTAAAAGATTTCCTGGAATGACAATTATATATTTTAACT-TTGGTGGGGAAANAGTTATAGGA 30 40 50 60 70 80 90 TTCTTCATTCAGAAAATTATCGGGCCA 310 320 330 340 350 360 370 CCACAGICTICACTICIGATACTIGIATITATIGCACTIGITITICACCATTAAGCTATATGIT AAAACAAACAAAAAAAAAAAAAA 140 150 160 170 180 190 200 AAAATTTTTTTTTTTTGAGAGCTTCTTATCAAAAGTAATGCTGCCAAAGGAAGTCTAAGGAATTAGTA 2.65 235 0 Optimized Score = 138 Significance Matches = 148 Mismatches Conservative Substitutions US-09-030-606-223 (1-383) US-08-806-596-39 Sequence 39, Application US/08806596 CACTTGTTTTGACCATTAAGGTATATGTTTAAAA 378 6 11 11 11 110 Initial Score Residue Identity Gaps 09E X TAATGGG 360 X

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us-09-030-606-223.res

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GCCTAGTT .
                                                                                                                                                                                                                                                                                                                                                         380 X
TAAAA
                                                                                                                                                                                                                                                                                                                                                                     GAGGGAACTTTTGGGCCTTTTTTCTTTTCTGTAGGCCGCCTTAAGCTTTCTAAATTTGGAACATCTAAG
150 160 170 180 190 200 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTGGGGGTTCCCTCCCANACCAACCCCNCTGACAAAAAGTGCCNGCCTCAAATNATGTCCCGGCNNTCN 370 400 400 410 420 430
                                                                                                                                                                                                                                                             170 220 230 230 CA----AAAGTAATGCTGCCAAAGGAAGTCTAAGGAATTAGTAGTGGTCCCMTCACTTGTTTGGAGTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 40 50 60 70 80 90
TTCTTCAGAAAAATTATCTTAGGACTGATATTGGTAATTATGGTCAATTTAATWRTRTTKTGGGGCA
                                                                                                                                                                                                                240 250 260 270 280 290 300 TATTCTAAAAAGATTTCCTGGAATGACAATTATATATTTTAACT-TTGGTGGGGGAAANAGTTATAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 320 330 340 350 360 370 CCACAGTCTTCACTTCACTTGAAGCTATAAGCTATATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.65
235
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.65
                                                                                                                                Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 Significance
148 Mismatches
                            | ||
TTGAAACACACNGAANGTTCTCATTNTCCCCNCNCCAGGTNAAAATGAAGGG
440 450 460 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGAAACACACNGCNGAANGTTCTCATTNTCCCCNCNCCAGGTNAAAATGAAGGG 440 450 450 460 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-383)
Sequence 39, Application US/09020747
                                                                                                      Sequence 39, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score = 138
Matches = 148
Conservative Substitutions
                                                                                                                              Optimized Score = 138
Matches = 148
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55
378
6
                                                                                                                                55
378
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10. US-09-030-606-223
US-09-020-747-39 (
                                                                                         9. US-09-030-606-223
US-08-904-809-39
                                                                                                                             Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score = Residue Identity =
380 X
TAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 X
TAAAA
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CTTGGGGGTTCCCTCCCCANACCAACCCCNCTGACAAAAGTGCCGCCTCAAATNATGTCCCGGCNNTCN 370 370 420 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATTGTTTTTTGAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 110 120 130 130 140 150 160 TITCCTTACATTGTCTTAGAAATGTCTTATTTGTAAAATTTTTGTATTTTGACAAGACTTCTTAT
                                                                                                                                                              70 180 190 200 210 220 230 CA----AAAGTAATGCTGCCAAAGGAAGTCTAAGGAATTAGTAGTGTTCCCMTCACTTGTTTGGAGTGTGC
                                                                                                                                                                                                                                                                      240 250 260 270 280 290 300 TATTCTAAAAGATTTTCCTGGAATGACAATTATATATTTTAACT-TTGGTGGGGGAAANAGTTATAGGA
                                                                                                                                                                                                                                                                                                                                                                                  310 320 330 340 340 350 CCACAGTCTTTGAATTTATTGCACTTGTTTTGACCATTAAGCTATATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 30 40 50 50 K 70 80 CAAAAAACAATTCTTCAGAAAATTATCTTAGGGACTGATATTGGTAATTATGGTCAATTTAATWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGACTICTTATCAAAAGTAATGCTGCCAAAGGAAGTCTAAGGAATTAGTAGTGTTCCCMTCACTTGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \begin{array}{c} 1.99 \\ 218 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Significance
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 X 240 250 260 270 280 AGTGTGCTATTCTTGATTTCCTGGAATGACATTATAACTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAAACACACNGCNGAANGTTCTCATTNTCCCCNCNCCAGGTNAAAATGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11. US-09-030-606-223 (1-383)
US-09-020-747-14 Sequence 147, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12. US-09-030-606-223 (1-383)
US-09-020-747-11 Sequence 115, Application US/09020747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score = 65
Matches = 70
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Optimized Score = 121
Matches = 138
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
368
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
378
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Score
Residue Identity
Gaps
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 360 x 370 380
ACTIGITITGACCAITAAGCTATATGITIAAAA
III I I
TIGAAGTITAGIC
X

13. US-09-030-606-223 (1-383) US-09-020-747-13 Sequence 136, Application US/09020747 Initial Score = 47 Optimized Score = 113 Significance = 1.99
Residue Identity = 30% Matches = 122 Mismatches = 258
Gaps = 3 Conservative Substitutions = 0

14. US-09-030-606-223 (1-383) US-08-806-596-12 Sequence 12, Application US/08806596 Initial Score = 47 Optimized Score = 127 Significance = 1.99
Residue Identity = 35% Matches = 144 Mismatches = 232
Gaps = 12 Conservative Substitutions = 0

15. US-09-030-606-223 (1-383) US-08-806-596-3 Sequence 3, Application US/08806596 Initial Score = 47 Optimized Score = 129 Significance = 1.99
Residue Identity = 35% Matches = 138 Mismatches = 245
Gaps = 2 Conservative Substitutions = 0

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100	250 260 270 280 290  IAAAAGATTTGATTTCTGGAATGACAATTATATTTAACTTTGGTGGGGGAAANA	X AAA    ACCTEGGCGTTACCAACTTAATCGCCTTGCAGCACTTTCGCCAGC	Intial Score = 47 Optimized Score = 129 Significance = 1.99  Residue Identity = 35% Matches = 138 Mismatches = 245  Gaps = 2 Conservative Substitutions = 0	X 10 20 AAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	30 40 50 60 70 80 90  AATTCTTCAGAAAAATTATCTTAGGGACTGATATTGGTAATTA-TGGTCAATTTAATWRTRTTKTGGG	100 110 120 130 140 150 160  GCATTICCTTACATTGECTGACAAGATTAAAAT-GICTGECCAAAATTIGTATTITATTIGGAGACTIC	170	240       250       260       270       280       300         ATTCTAAAGATTTCCTGGAATGACAATTATATTTAACTTTGGTGGGGGAAANAGTTATAGGACCACAACTTTTGGTGGGGGGGAAANAGTTATAGGAACGTGCTCCACCAACATCTTTTGGTGGGGGGGG	310 320 340 350 360 380 380 380 380 370 370 380 ACAGTCTTCACTTCACTTGACCATTAAGCTATATGTTTA CACTTTGACCATTAAGCTATATGTTTA CACTTTGACCATTAAGCTATATATATATATATATATATAT

TGGGCGTTACCAACTTAATCGCCTTGCAGCACATCCCC 500  TGGGCGTTACCAACTTAATCGCCTTGCAGCACATCCCC 500  9-030-606-223 (1-383) 9-020-747-3 Sequence 3, Application US 5core	470 480 490 GGCCAGC	20747  29 Significance = 1.99  88 Mismatches = 245  88 November = 245  80	AIGHIGANCANCICICAAAAGI 110 120 130 70 80 90 A-TGGTCAATTTAATWRRTTKTGGAAA 30 150 160 ATTTGTATTTATTTGGAGACTT 1	220 230  ITCCCMTCACTTGTTTGGAGTGTGCT	STTTGACCATTAGCTATATGTTT	US/08904809  142 Significance = 1.82 154 Mismatches = 229  tutions = 0  40
X	460 ATCCCCCTTTC	ion US/090207 re 129 138 Substitutions	100 100 ATTGGTAATTA ATTGACACCA 70 130 14 PTCTGTGCCAAA TCTGTGCCAAA	210 ATTAGTAGTGT	TATTGCACTTG	re = 142 154 Substitutions OCATTCAGAAAAAT 1
X AAA  CCCTGGGCGTTACCAACTTAATC X 500 510 510 510 510 510 510 510 510 510	450 GCCTTGCAGCAC 520	) 3, Applicat ptimized Sco latches conservative	SO SO STEGGGACTGAT STEGGCGTCAAG 160 120 LAGATTAAAAT-G TCTGGCCAATCA	200 GAAGTCTAAGGA 1   1   1   1   1   1   1   1   1   1	AAATTAATCTTT	', 'e 46, Applic Ptimized Sco latches Conservative 20. 3 AAAACAATTCTT (CCAGATCTATGA
AAAACA  AAAAACA  AAAAACA  AAAAACA  AAAACA  AAAAACA  AAAACA  AAAAACA  AAAACA  AAAACA  AAAACA  AAAACA  AAAAACA  AAAACA  AAAACA  AAAACA  AAAACA  AAAAACA  AAAACA  AAAAACA  AAAACA  AAAAACA  AAAAC	440 CCAACTTAATC 510	-223 (1-383 -3 Sequence 47 0 = 35% M	40 GAAAATTATC CACAGGCATCT 150 110 110 TTGTCTTGACA TTGTCTTGACA 1111	180 TGCTGCCAAAG TGATCAGCAGC 10 260 TTGATTTCCTG 1         1         TTGTATAGAAA TTGTATAGAAA	CTGATACTTGT             TANTGAGTCGT   440   CCAACTTAATC   510	-46 Sequenc - 45 O - 38% M - 8 C 10 AACAACAAAA           ATGTTATAAG
	X AAA     ACCCTGGGCGTTA X 500	17. US-09-030-606 US-09-020-747 Initial Score Residue Identity Gaps	30 ATTCTTCATCA ATTCTTCATTCA 1	170 TTATCAAAAGTAA	ACAGTCTTCACTT	Initial Score Residue Identity Gaps  X AAAACA ACTITITATTAA

Thu May

us-09-030-606-223.res

  TGCCTTACTCTTTGGG 440 19. US-09-030-606-223 (1-383)
US-09-020-747-46 Sequence 46, Application US/09020747

Initial Score - 45 Optimized Score - 142 Significance = 1.82
Residue Identity - 38% Matches - 154 Mismatches - 229
Gaps - 8 Conservative Substitutions - 0

  20. US-09-030-606-223 (1-383) US-08-904-809-59 Sequence 59, Application US/08904 Initial Score = 44 Optimized Score = 112 Significance = 1.74
Residue Identity = 37% Matches = 122 Mismatches = 186
Gaps = 5 Conservative Substitutions = 0

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us-09-030-606-177-inv.res made by tport on Thu 1 May 103 15:08:41-PDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    initial comparison of US-09-030-606-177' (1-1119) with:
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The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

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g. Fr	14	9 7 4 4 8 4 8 8	4 4 6 E E E	12	96	96.9	96	96.96 98.88		.14	ACATT	AATGA     AGTAC 90	410 AGAAATTATGTG A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	FTGAG       VTCCG	raatc etggg	620 GCAG
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Opt. Score		239 158 217 217	217	37	68 80	114 179	174 174	242 242 242 103	-	cance =	X 250 260 AATGGGAACACGATCATACATT	330 ACAACAGGAGAAATGA 	400 GTCAGAA     GCCCTTT	460 470  AACTGGATACCAAGATGGTTGAG	540 STCAACA         TGCAGGG	610 FGATGCA
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	deviations Application	Application Application Application Application	Application Application	lication plicatio lication	/lation lication lication	, Application Application	Application Application	lication lication lication plicatio	Application US,	Score =	230 3GATTTAAAGGCT	310 3GCTCCAGAGGCGC 1                     TAAAGCGGGCGC	380 AGCTATATGATCCCTCAC	450 ATTCAGTGAGGAT             ACTCGTGTATTTT	510 520 530 540  AAACATCGCATGGTTAGTACAATAGACAGCACAGTCAACACAGTAATC	590 FGCTAGTTGATC
ription	** 3 standard Sequence 37, P	Sequence 37, Sequence 106 Sequence 39,	Sequence 39, Sequence 177	Sequence 40, Sequence 110 Sequence 79,	** 1 standar Sequence 12, Sequence 12,	Sequence 139 Sequence 69,	Sequence 74, Sequence 74,	Sequence 32, Sequence 32, Sequence 32, Sequence 145	(1-1119) equence 37, App	69 Optimized So 36% Matches 27 Conservative	200 210 220 230 240 x 250 260 AGACCTGCCTGGTGCTTGAGGGTTTAAAGGCTTTGGGTAATGGGAACACGATCATACAT A A A A A A A A A A A A A A A A A A A	270         30         310         320         330           CATCATTGTGACCCCCCCCCCCCCCCCCCCCCTTCCACACCACCACACACACACACACACACACACACACACAC	40         350         360         410         410           ATTIGIGAGGGAGTACCAGCATCCTTGAAGAGCTATATGATCCTCACCTCTGTAGGTCAGAAATTATGTG         1   1   1   1   1   1   1   1   1   1	420         430         440         450         460         470           GGAATGGCTGACACTGAATTCAGTGAGGATAACTGGATACCAAGATGGTTGAG         1   1   1   1   1   1   1   1   1   1	500 510 520  CACCTAAACATCGGCATGGTTAGTACAAT	0 550 570 580 590 620 ATGATAGTTCACAGTGTTCCGGGTGATGCAGTGAGCAG
Descr	*** 06-596-37	7000	747-3	-809-4 -747-1 -747-7	*	1.0	7	-806-596-32 -904-809-32 -020-747-32	606-177′ 596-37 S	ity =	210 GCCCTGGTG	280 TGTGACCTGCAC.            TGTTGCCATAAC. 30 40	350 GGGAGTACC GATGCTCTCC	GACACTGAA GACACTGAA           TGCGCTGGA	490 CGCTAATT1 	60 TGACTTCGG
Sequence Name	1. US-08-8	S-08 S-09 S-08	. us-09	80-SD .	1. US-09-	3. US-09-	5. US-08- 6. US-09-	17. US-08-8 18. US-08-9 19. US-09-0 20. US-09-0	1. US-09-030- US-08-806-	Initial Score Residue Identi Gaps	200 GCTAGACCT	270 CATCATTGT        TGTTCTTGT 30	340 350 ATTGTGAGGGAGG I I I I I CAGCGCGGGATGCT	420 GGAATGGCTG        GGAAATGGAT	480 GCCAAGTGA           GGCAGTTGG	550 ATGATAGTC

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	630 640 650 660 670 680  TAGTGAGCACCCAGTGAGGATGCAGCAGGACGTCCTTGCACTGGAAGTTGCCGAAATGGTACAAC	690 700 710 720 730 740 750 CTGCCAGGGTTGGAAAGCTTCTCACACTCCCACAGTCTGGGACTGGATGGCAATCACAGCAT TTGTTGGTTGGGACTGGAATGCCATAGCATTGTTGTTGCCCAAAGCAACCAAAAACTTGCAAAAATCTGCTCCGTGGGGGTCATNNNTACCAAAAATCTTGTTGCCCAAAGCAACCAAAAAAAAAA	760         770         780         790         800         810         820         830           CGTTCGCCAGCAGACCAGCCAGGAAACGAGCAAACGAAGCAAAACCAGAAAACCAGAAAAAA	840 850 860 870 880 890 900 . TGCTCCGGATGGTGTCAGACTCGGACACGGATTCGTCCAACTTGATGAGCATGAGGTCGTTAGCGAGCAAGG

GT - - CTGTTGTACTCTGGGTGCCGTACGGAGGCTGGCCTCCACCATCTGGCTCCCTGGCTCTTGGTCGGC TTGGGTGGAANAGCACAATTGAACTGTTAACNTTGGGCCGNGTTCCNCTNGGGTGGTCTGAAACTAATCACC 590 640 650 GTCACTGGAAAAAGGTANGTGCCTTCCTTGAATTCCCAAANTTCCCCTNGNTTTGGGTNNTTTCTCCTCTNC 680 690 710 710 720 CGGATGCAC

2. US-09-030-606-177' US-08-904-809-37 S

' (1-1119) Sequence 37, Application US/08904809

2.98 462 0 Significance Mismatches Optimized Score = 239
Matches = 284
Conservative Substitutions 67 36**8** 27 Initial Score = Residue Identity = Gaps

480 490 500 510 520 530 540 GCCAAGTGACGACAGAATAGACAGACACAGTAATC 0 560 570 580 590 600 610 620 ATGATAGTTCACAGTGTTCCGGGTGATGCAGTGAGCAG 650 660 670 680 ----TGCAGGACGTCCTTGCACTGGAAGTTGC--CGAAATGGTACAAC TTCTTGTTGCCCAAGCANCCTCCANCAAACCAAAANCTTGCAAAATCTGCTGGGGGTCATNNNTACCA 840 850 860 870 870 900. TGCTCCGGATGGTGTCAGACTCGTCCAACTTGATGAGCATGAGGTTAGCGAGCAAGG 690 700 710 720 730 740 750 CTGCCAGGGTTGGGAATGGCAATCACAGCAT 760 770 780 790 800 810 820 830 CGTTCGCCAGCAGCCAGCAAGAAGCAAGAGCAAGAGTTCCCCGCGGTAGGGCACTGCGAAGCAATGCTGA 910 920 930 940 950 970 970 950 960 970 970 960 970 970 970--CTGTTGTACTCGGGGGGGGGGGGGCTCCACCATCTGGTCGGG CTCAAGACTGTGCAGGCCCAGCCCGATGGTGTAGGAGTTCTGGAAACAGTGTGCGGCTGACAGCACCCACTG 200 CCTAAAAATCGTNTTCCCCCCCCNTANGGCG 730 740 750 630 640 TAGTGAGCACCCAGTGAGGA-

CGGATGCAC

3. US-09-030-606-177' (1-1119) US-09-020-747-10 Sequence 106, Application US/09020747

2.74 276 0 Significance Mismatches Optimized Score = 158
Matches = 192
Conservative Substitutions 64 38% 34 Initial Score Residue Identity

TTTTTTTTTTTTAGTCAA

us-09-030-606-177-inv.re

3/0	TTGAAGA	=======================================	TCCAAGA	0		
360	CAGCATCC	=	TATATTCC	160	•	
350	SGGGAGTAC	=======================================	ATTGAGTAA	150		
_	TTGTGA(	_ =	GTGCCATT	140		
340	GAAATGAAT	= =	AAATGTAAG	130		
330	CAACAGGA	Ξ	CAATTTAT	120		
320	TTTCACTA	<del>-</del>	ACAACTGTA	110		
310	TCCAGAGGGCGCACCTTTCACTACAACAGGAGAAATGAATTTGTGAGGGGAGTACCAGCATCCTTGAAGA	<del>-</del>	<b>AAGAAACGTTTTAGACAACTGTACAATTTATAAATGTAAGGTGCCATTATTGAGTAATATATTCCTCCAAGA</b>	100 13		
	TCC		AAG	. •		

730 740 CAGTCTGGGACTGGAT

'' (1-1119) Sequence 39, Application US/08806596 4. US-09-030-606-177' US-08-806-596-39 St

2.43 513 217 Significance 233 Mismatches Conservative Substitutions 8 8 Optimized Score Matches 308 308 Initial Score
Residue Identity Gaps

TTTTTTTTTTTTTGCT X 10 20

280

US-09-030-606-177' (1-1119) US-08-904-809-39 Sequence 39, Application US/08904809

2.43 513 0 217 Significance 233 Mismatches Conservative Substitutions Optimized Score Matches 60 30% 9 Score Identity Initial Residue Gaps

 | 790 | 800 | 810 | 820 | 830 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 840 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 850 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860

| 860 | 870 | 880 | 900 | 910 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920 | 920

6. US-09-030-606-177' (1-1119) US-09-020-747-39 Sequence 39, Application US/09020747

Initial Score = 60 Optimized Score = 217 Significance = 3 Residue Identity = 30% Matches = 233 Mismatches = 6aps = 9 Conservative Substitutions =

     | 790 | 800 | 810 | 820 | 830 | 840 | 850 | 840 | 850 | 840 | 840 | 850 | 840 | 840 | 850 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 860 | 840 | 860 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840 | 840

7. US-09-030-606-177' (1-1119)
US-09-020-747-17 Sequence 177, Application US/09020747

Initial Score = 60 Optimized Score = 148 Significance Residue Identity = 34% Matches = 158 Mismatches Gaps = 4 Conservative Substitutions

	•	
. 06	CAGCTICTGTTTATTAAGCACCTAATGTGTTACAACTGCACAGATCCCATTGAACCATGGGCCCTCTCCCTC	
80	CCATGGGCC( 	
.70	CCATTGAAC        TGAGGGATC 740	
٠.	TGCACAGATCC         CCTACAGAGGT0	11
09	TACAACTG	
20	TAATGTGT   	
40	TAAGCACCTV    GCCATTCCCV 710	
30	CTGTTTAT          CAGTGTCA 700	
	CAGCTT         CTGCTT 690	

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8. US-09-030-606-177' (1-1119) US-08-904-809-40 Sequence 40, Application US/08904809 Initial Score = 58 Optimized Score = 234 Significance = 2.27
Residue Identity = 35% Matches = 275 Mismatches = 474
Gaps = 29 Conservative Substitutions = (

CTCCGGGTGACAGCCGCGCGTCGGCCAGGATCTGAGACGTGTCCCCACTGAGGTGCCCCACAG $30 \qquad 40 \qquad 50 \qquad 60 \qquad 70 \qquad x \qquad 80 \qquad 90$ 

X 10 20 TTTTTTTTTTAACATCA

2.12 680

Significance Mismatches

Optimized Score = 372 Matches = 431 Conservative Substitutions

Initial Score Residue Identity Gaps

9. US-09-030-606-177' (1-1119) US-09-020-747-11 Sequence 110, Application US/09020747

g

230	0 TGCAG       GGTCG 300	CAAC 	GCAT	830 CTGA 111 ICTGG 500	900 GCAAGG   GGTTNT 570	970 TCGGCC       TGNNAC 0	CTGC    TCCC	GTGC
	550       560       570       580       590       600       610         TAATCATGATCATGATGCTGCTAGTTGATCACAGTGTTCCGGGTGATGCAG         I	620         630         640         650         670         680           TGAGCAGTGCAGGACGTCCTTGCACTGGAAGTTGCCGAAATGGTACAAC           I I I I I I I I I I I I I I I I I I I	690 700 710 720 730 740 750 CCTGCCAGGGTTGGAAAGCTTCTCACACTCCCAGCTCCCACAGCATCGGATGGCAATCACAGCAT III	60         770         780         830         830           CGTTCGCCAGCCAGACAGCCAAGAGTTCCCCGCGGTAGGGCACTGCGAAGCAATGCTGA         1 <td< td=""><td>840         850         860         870         880         890         900           TGCTCCGGATGGTCTCGGACACGGATTCGTCCAACTTGATGAGGTCGTTAGCGAGCAAGG         1</td><td>910 920 930 940 950 960 970 GTCTGTTGTACTCGGGTGC-CGTACGGAGGCTGGCTCCACCATCTGGCTCCCTGGCTCTTGGTCGGCC</td><td>980 990 1000 1010 1020 1030 1040  TCAAGACTGTGCAGCCCGATGGTGTAGGAGTTCTGGAAACAGTGTGCGGCTGACAGCACCCACTGC   </td><td>1050 1060 1070 1080 1090 1100 1110 GGATGCACCAGGACGCAGAGAACAATTCGTTTTCCATGACCAGTGCCGCCTGCCAGGGCTGCGAGTGC</td></td<>	840         850         860         870         880         890         900           TGCTCCGGATGGTCTCGGACACGGATTCGTCCAACTTGATGAGGTCGTTAGCGAGCAAGG         1	910 920 930 940 950 960 970 GTCTGTTGTACTCGGGTGC-CGTACGGAGGCTGGCTCCACCATCTGGCTCCCTGGCTCTTGGTCGGCC	980 990 1000 1010 1020 1030 1040  TCAAGACTGTGCAGCCCGATGGTGTAGGAGTTCTGGAAACAGTGTGCGGCTGACAGCACCCACTGC	1050 1060 1070 1080 1090 1100 1110 GGATGCACCAGGACGCAGAGAACAATTCGTTTTCCATGACCAGTGCCGCCTGCCAGGGCTGCGAGTGC
220	O TTCCG       ATNAG 290	GCCGAA 11 NAATAA 60	TGGCA TACCCA	820 GCGAA( TGATG( 490	890 rcgrra   1 NTTTCA 560	960 TGGCTC     1 TNCCCC	GACAG	1 CAGGG
0	600 AGTGT       	670 AAGTTG 	740 ACTGGA 11 : GCTCNA 420	SGCACT        TCTNC	rGAGG'I       rcctcn	9 CTCCCT         CACCHT  630	1030 3CGGCTC 	1100 GCCTGC
210	ATCAC	0 CACTGG/          C CGCAGG/ 350	CTGGG1       GTTGG(	810 GGTAGGG I TGGGCTS	880 GAGCA1     CCNCC1 550	950 TCTGGC NTACTC	O AGTGTC   CTTNCA	grecco
0	590 AGTTGI I CACCG	660 CTTGC2 11   CTCCC	730 ACAGT   ATGAN 410	O CCCGC GNTCT	TTGAT   ANCAC	CACCATO	1020 GAAACA(   ANANGC: 690	1090 GACCA
200	TGGCT       CGACA 270	) ACGTC         AGGGC	CTCCC	800 3AGTTCCC       TCTTCGI	870 CCAAC      CCTAA	940 TGGCCTC      ATATCTC 610	.0 STTCTG       SNTCAA	TCCAT
190	550 560 570 580 590  TAATCATGATAGTCTGGAGAACTATGGTGCTGGCTAGTTGATCAC-	650 AGCAGG/ 1 3CTGGC/ 3A	720 CCCAGC   rctcnP 400	790 AGGCAAG I CCAAATC 60	ATTCGI     CGGGGI	AGGCTG   NCCCAT	1010 TAGGAGTT     FGGCCCNT	1050 1060 1070 1080 GGATGCACCAGGACGCCGAGCAGAACAATTCGTTT
Ä	0 AACTA5 I CAACN	O GATGC I TGGGA( 330	ACACT(           	79( AACGAG(   ATTCCC/ 460	860 CACGG 1 ANCCC( 530	930 ACGGAGA        AAGGGAA 600	1000 GATGGTG' CGNCCTC'	ACAAT'   TGTCT
180	570 CGGAGAJ I I I	640 GTGAGG	710 TTCTC 	780 AGCCAGA 1 11 TGANGGA	TCGGA        CCCCA	-cgra     TCTCA	100 ICCCGA7       NCCCGI	1070 NGCAGAA     NCNTT: 740
7	560 CTGACTT          CAAAGTT	630 GCACCCA I TGGCGTC 320	SAAAGC	7 SCCCAG 11 1 FCCTTG	850 FCAGACY AANCAN	920 GGGTGC 	990 GCCCAG NTTCCC	SCCCGP SCCCGP
170	TAGTC7 TAGTC7 1 11 TTCTC2	6. GTGAG( GTGAG( GTGGT(	700 GTTGG( 1	770 AGCAGA(   1 CGGACT	0 TGGTG:   ATGCC!	ACTCT(       ACCNT(	TGCAGGG	1060 AGGACGC   ATCTGNZ 730
	550 TCATGAT	620 GCAGTA   ATAANC	690 700 CCTGCCAGGGTTGG 	CGCCA   -NNCC	840 CCGGATC      CCNGNA' 510	910 GTTGT   CCCCGG	980 GACTG	O GCACC       NCCCT
160	TAAT	6 TGAG GTCA	690 CCTG 1 1 1 CCCG	760 CGTT	TGCT   TTGC	GTCT	90 TCAAGA       CCANCO	1050 GGATG   CCCTN 720

us-09-030-606-177-inv.res

 | 810 | 820 | 830 | 840 | 850 | 860 | 870 | 860 | 870 | 860 | 870 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870

1010

AGGCGTTCGGATGG

10. US-09-030-606-177' (1-1119) US-09-020-747-79 Sequence 79, Application US/09020747 Initial Score = 55 Optimized Score = 176 Significance = 2.04
Residue Identity = 35% Matches = 213 Mismatches = 339
Gaps = 44 Conservative Substitutions = 0

  (1-1119) Sequence 12, Application US/09071710 11. US-09-030-606-177' US-09-071-710-12 Se

Optimized Score = 89 Significance = Matches = 94 Mismatches = Conservative Substitutions = Optimized Score 328 1 Initial Score
Residue Identity = Gaps

TAACATCACAGCTTCTGTTTATTAAGCACCTAATGTGTTACAACTGCACAGATCCC X TTTTTTTTTTT

12. US-09-030-606-177' (1-1119) US-09-525-397-12 Sequence 12, Application US/09525397

TITITITITITITITAACATCACAGCTICTGTTTATTAAGCACCTAATGTGTTACAACTGCACAGATCCC 1.96 Optimized Score = 89 Significance = 94 Mismatches = Conservative Substitutions = -Optimized Score Matches 54 328 1 Initial Score Residue Identity Gaps

US-09-030-606-177' (1-1119) US-09-020-747-13 Sequence 139, Application US/09020747

1.96 225 0 Significance Mismatches Optimized Score = 114
Matches = 135
Conservative Substitutions 54 36% 8 0 0 0 Initial Score
Residue Identity = Gaps

 14. US-09-030-606-177' (1-1119) US-09-020-747-69 Sequence 69, Application US/09020747

1.96 341 0 179 Significance 194 Mismatches Conservative Substitutions Optimized : Matches 354 354 5 Initial Score
Residue Identity Gaps

```
80 90 100 110 120 130 140 TGAACCATGGGCCCTCTCCCTCACCTCCCCAAGGAGCAGCATGCAGGAGCTCAACTAGGCAGAGAATCCAG
                                                        ACTAGTCCAGTGTGGTGGAATTCCAT
X
                                                                                                                                                                         220 230 240 250 260 270 280 GAGCATGAGGGATTTAAAAGGCTTTGGGTAATGGGAACACGATCATACATTCATCATTGTGACCTGCACACCC
```

580 x 590 600 610 620 630 GGTGCTGGCTGGCTGAGTGAGCACCCAG x 590 | ||| | GTTGCCAGGC 530 X

174 Significance 203 Mismatches 15. US-09-030-606-177' (1-1119) US-08-904-809-74 Sequence 74, Application US/08904809 Optimized Score Initial Score = Residue Identity = Gaps = -

1.96 331

Conservative Substitutions

16. US-09-030-606-177' (1-1119) US-09-020-747-74 Sequence 74, Application US/09020747

 $\frac{1.96}{331}$ Optimized Score = 174 Significance = Matches = 203 Mismatches = Conservative Substitutions = 54 368 20 Initial Score Residue Identity Gaps

										•			
_ <del></del>					· ¥ ·				,	:			
230	0 GCACAGTC     1 4  TTA-GGGC 300	CCGGGTGA       CTTGATAT 370	680 GAAATGGT        AATGAT	750 GCAATC 	820 GCGAAGCA			1.96	70 NGATCCCAT      TTNCCNAG	140 NGAATCCAG       SGCGGCGGC	210 TGGTGTACT      CTGCAGCTG	) GCACACCC     TITNAATTT 260,	350 GGGAGTACC           CGTTGGCNC
220	CAATAGACA CAATAGACA 11 11 NTGGTAATCA	600 CCACAGTGTT        TCCAGTTTG	670 3GAAGTTGCC   	740 3GACTGGATG           3AAAATGAAG	810 STAGGGCACT	• •		Significance = Mismatches =	60 2AACTGCACA      TTTTTTTT	130 ACTAGGCAG?      ACAGGCTCCC	AGACCTGCCCT	270 280 ATTCATCATGTGACCTGCACCCC	90         310         320         330         340         350           ACCCTGGGAGGCTCCAGGGCACCTTTCACTACAACAGGAGAATTTGTGAGGGAGTACC         - GTGAGGGGAGTACC         - GTGAGGGAGTACC         - GTGAGGGAGTACC           1   1   1   1   1   1   1   1   1   1
210	52C ATGGTTAGTA 	590 SCTAGTTGAT        FATACTGCCT	660 CCTTGCACTG      NCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	730 2acagrcrgc 	800 rrccccccc		38806596		50 AATGTGTTAC 	120 CAGGAGCTCAA        CAGGACGGCAA 120	SAAATGCTAC	270 ACATTCATC? 	3.40 AATGAATTT-
	S10 AACATCGGCZ 	580 ATGGTGCTGC       ATGGTAGTT	650 SCAGGACGTO      ATGGGTTCTA	720 CCAGCCTCCC 	790 AGGCAAGAG		Application US/08806596	= = ostitut	40 raagcaccii   	GGCAGCATGC/                 GGCTGGGGAC/ 110	190 CTAAATGAAG, I   CAGCCTCCGC'	260 CACGATCATI	330 AACAGGAGA        ATTAGGAAT
	500 TTTCACCTAA	570 CGGAGAACTI      NTACTAAATT	640 SAGGATGCA(     NTATTTTGA/ 410	710 TCTCACACTCC 	780 GCCAGAAACGI I GT X			Optimized Score Matches Conservative Sul	30 PCTGTTTAT:               TTTTTTTT: 30	110 CCCAAGGAGGC CCCAAGGAGGC 1	180 CAGCATACAO       CCAAATNTGO	250 FAATGGGAA(       CNTNGG	320 TTTCACTACA       CACCACCNI 300
	490 GACGCTAAT           \GACTCTGAT	560 STCTGACTTC       GGGTACTT	630 GCACCCAGTC   1 TCTTGACTT/	) 3GAAAGCTTC 	0 AGACCCCAGG             AAAGTCCCG		/ (1-1119) Sequence 33	54 Optimiz 34% Matches 43 Conserv	20 ATCACAGCT:         TTTTTTTTTTTTTTTTTTTTTTTTTTTTT	CCTCACCTCCC	170 ATGAATGGA(       1	240 GGCTTTGGG'          GGCCTCGGC	310 ' 366C6CACC'          36CANCCCC' 290
0	480 3AGGCCAAG1 11 1 AAGAATTAC? 250	550 ATCATGATAC 	620 GCAGTAGTGAC GCAGTAGTGAC 1   1 ATATTAAGAT1	700 CCAGGGTTGG   1 AAGACATCGA	0 GTTCGCCAGCA GTTCGCCAGCA I I I I I I I I I I I I I I I I I I I		-606-177' -596-32 Se	D B 8	0 rtrtttaac        rtrttrtr	90 GGCCTCTCC I ATTGACAACC	160 3GTGGTTGC/ 1	230 GGGATTTAAA(       CNTAAAACAG( 220	300 .GGCTCCAGA(       .CAATGCGGT(
170	470     480     490     500     520     530       AAGATGGTTGAGGCCAAGTTCACCTAAACATCGGCATGGTTAGTACAATAGACACCACAGTC     11	540         550         560           AACACAGTAATCATGATAGTCTGGAGAACTATGGTGCTGGCTAGTTGATCACAGTGTTCCGGGTGA         1   1   1   1   1   1   1   1   1   1	SCAGTGA     TTGTTG	690 700 710 720 730 740 750 750 740 750 750 740 750 750 750 750 750 750 750 750 750 75	76 CAGCATC      CAAATTG	ATGCTG	US-09-030-606-177' (1-1119) US-08-806-596-32 Sequence 32,	nitial Score esidue Identity aps	X         10         20         30         40         50         60         70           TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	80         90         100         110         120         130         140           TGAACCATGGGCCCTCTCCCTCACTCCCCAAGGAGCTCCAGGAGATCCAG         1 <td>  150</td> <td>220 AGCATGA        AGGATGC</td> <td>290         310         320         330         340         350           ACCCTGGGAGGCTCCAGAGGGGCACCTTTCACACAGGAGAATGATTTGTGAGGGAGTACC         1   1   1   1   1   1   1   1   1   1  </td>	150	220 AGCATGA        AGGATGC	290         310         320         330         340         350           ACCCTGGGAGGCTCCAGAGGGGCACCTTTCACACAGGAGAATGATTTGTGAGGGAGTACC         1   1   1   1   1   1   1   1   1   1
		aria w	610 T		A	• •	7. 1	nitial esidue aps	•			G. C. 210	7

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CCCAAATCCTCCCCCGNTTNCTGGGTTTGGGAACCCACGCCTCTNNCTTTGGNNGGCAAGNTGGNTCCCCC 630 640 650 660 670 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCGGGCCCCGGTGGCCCNNCTCTAANGAAAAC---NCCNTCCTNNNCACCATCCCCCCNNGNNACGNCT 720 730 740 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 80 | 100 | 110 | 120 | 130 | 140 | 140 | 140 | 150 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 100 | 130 | 130 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 | 140 |
                                                                                  650 660 670 680 690 700 710 AGCAGGACGTCCTTGCACTGCGAAAGCTTCTCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720 730 740 750 760 770 780 CCCAGCCTCCCACAGCAGCAGCAAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 800 810 820 x 830 840 850 860 GGCAAGAATGCTGATGCTCCGGATGGTGTCAGACTCGGACACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X 10 20 30 40 50 60 70 TITITITITIAACATCACAGCITCIGITITAAGCACCAGATGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 370 380 390 400 410 420 AGCATCCTTGAAGATCCTTGACGTCACACTGAAATTATGTGGGAATGGCTGACACTGAA
                                                                                                                                                                                                                                                                                                                                                            TTGGTTANTNTNCCNGCCACAATCATNACT----CAGACTGGCNCGGGCTGGCCCCAAAAAANCNCCCCA 410 420 450 450 460 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.96
497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Significance = Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-030-606-177' (1-1119)
US-08-904-809-32 Sequence 32, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimized Score = 242
Matches = 288
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANCAANGNATCCCTTTTTANAAACGGCCCCCCNCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348
43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTCGTCCAACTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.
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		\$ ·				
CAGGATGCCNTAAAACAGGGCCTCGGCCNTNGGTGGGCACCCTGGGATTTNAATTT  210	430 440 450 460 470 480 490 500 6CAGGAAATCTCAATTCAGTGAGGATAACTGGATACCAAGTGGTGGCCAAGTGACGCTAATTCACCT	580 640  TATGGTGCTGGCTAGTTGATCACAGTGTCCGGGTGATGCAGTGAGCAGTAGTGAGCACCCAGTGAGGATGC	CCCAATCCTCCCCCGNTTNCTGGGTTTGGGAACCTTGCCAGGGTTGGGAAGCTTCTCACACTTGCCAATCCTCCCCCCCC	790 800 810 820 x 830 840 850 860 GGCAAGAGTTCCCCGCGGTAGGCACTGCGAATGCTCCGGATGGTCCAGACTCGGACACGG	19. US-09-030-606-177' (1-1119) US-09-020-747-32 Sequence 32, Application US/09020747  Initial Score = 54 Optimized Score = 242 Significance = 1.96  Residue Identity = 34% Matches = 288 Mismatches = 497  Gaps = 43 Conservative Substitutions = 0	X

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220 230 240 250 260 270 280 GAGCATGAGGGATTTAAAAGGCTTTGGGTAATGGGAACACGATCATAATGTGACTGCACACCC
                                                                                                                                                                                                                                                   390 340 350 350 350 350 ACCTTGGGAGGAGAATGAATTT----GTGAGGGGAGTACC
                                                                                                                                                                                                                                                                                        360 370 380 390 400 410 420 AGCATCCTTGAAGAGCTATATGAGCTGACACTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 160 170 170 180 190 200 210 GAGTCCTGAGGTGCTGCCTGCCTGGTGTACT
                                                                                                                                                                                            CAGGATGCCNTAAAACAGGGCCTCGGCCNTNGG-------TGGGCACCCTGGGATTINAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACCGGNCCATGTCTTNNCGGGGTTGCTGCNATNTNCA----TCACCTCCCGGGCNCANCAGGNCAACCCC 530 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  720 730 740 750 760 770 780 CCCAGCCTCCCACAGTCTGGATGGCAATCACAGCATCGTTCGCCAGCAGCAGCCAGAAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 800 810 820 x 830 840 850 860 GCCAGAGAGTTCCCCGGGTAGGGCACTGCGAAGCAATGCTGAGGATGGTGTCAGACTCGGACAGG
                                                                                                                                                                                                                                                                                                                                                                                          ACTCCCCNTGGAAACCACTINTCGCGGCTCCGGCATCTGGTCTTAAACCTTGCAAACNCTGGGGCCCTCTTT
340 350 360 370 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 520 530 540 550 560 570 AAACATCGCCATGGTTAGTACAATAGACAGACAGTCAACAGTAATCATGATAGTCTGACTTCGGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 440 450 460 500 GCAGGAAATCTGGATACCAAGTGGTTGAGGCCAAGTGACGCTAATTTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 590 640 TATGGTGCTGGCTAGTTGATCACAGTGTTCCGGGTGATGCAGTGAGCAGTAGTGAGCACCCCAGTGAGGATGC
  130
  120
  110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANCAANGNATCCCTTTTTANAAACGGCCCCCCCCCC
80
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103 Significance = 118 Mismatches =

Optimized Score = 103 Matches = 118 Conservative Substitutions

53 418 5

Initial Score = Residue Identity = Gaps

7' (1-1119) Sequence 145, Application US/09020747

20. US-09-030-606-177' US-09-020-747-14 Se

870 ATTCGTCCAACTTGAT

21. US-09-030-606-177' (1-1119) US-09-020-747-16 Sequence 164, Application US/09020747 Initial Score = 51 Optimized Score = 154 Significance = 1.72 Residue Identity = 35% Matches = 171 Mismatches = 297 Gaps = 10 Conservative Substitutions = 0

740 T 22. US-09-030-606-177' (1-1119) US-08-806-596-28 Sequence 28, Application US/08806596 Initial Score = 51 Optimized Score = 203 Significance = 1.72
Residue Identity = 31% Matches = 237 Mismatches = 490
Gaps = 21 Conservative Substitutions = 0

540 550 600 600 CACAGTCAACAGTAAGTCTGACTTCGGAGAACTATGGTGCTGGCTAGTTGATCACAGTGTTC CACAGTGTTC CACAGTGTTC CACAGTGTTC CACAGTGTTC CACAGTGTTC CACAGTGTTC CACAGTGTTC CACAGTGTTC CAGAGTAGTGCATNTTNGGGGGNCNGCCANGTTTCCCAGGCTGCTANAATCGTA 230 240 250 250 260 270 280 290

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CGCCTNGGGNAANCCTCCTGNAATGGGTAGGNCTTNTCTTTTNACCNNGNGGTNTACTAATCNNCTNCACG 590 640 650
 TGCTCCGGAT-GGTGTCAGACTCGGACACGGATTCGTCCAACTTGATGAGCATGAGGT
                                                                         890 900 910 920 930 940 950 CGTTAGCGAGAGGCTGGCCTCCACCATGGCTGGCTCCTG
                                                                                                                                                                                                     CNTNCTTTCTCNACCCCCCCTTTTTCAATCCANCGCCNATGGGGTCTCCCCNNCGANGGGGGGNNNCC 680 690 710 710 720
                                                                                                                                                                      250 260 270 280 290 x 300 310 GTAATGGGAACACGATCATCATGTGACCTGCACCCTGGGAGGCTCCAGAGGGCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 330 340 350 360 370 380 CTTTCACTACACAGGAAAATGAATTTGTGAGGGGAGTACCAGCATCCTTGAAGAGCTATATGATCCTCA ANGGGATTGATGATCCCTCA 370 380 370 380 380 370 380 380 380 380 380 380 380 380 80 80 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAAGGCCGGAGGGATATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 400 410 420 430 4*U
CCTCTGTAGGTCAGAAATTATGTGGGAATGGCTGACAGAAGCAGGAAATCTCAATTCAGTGAGGATAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 470 480 490 500 510 520 530
GGATACCAAGATGGTTGAGGCCAAGTGACGTTAGTTTCACCTAAACATCGGCATGGTTAGTACAATAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Significance = 1.72
Mismatches = 490
                                                                                                                                                                                                                                                                   X
GACAGCACCACTGCGGATGCACCAGGACGCCCGAGCAGAACAATTCGTTTTCCAT
                                                                                                                                                                                                                                                                                                                                                                             23. US-09-030-606-177' (1-1119)
US-08-904-809-28 Sequence 28, Application US/08904809
                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimized Score = 203
Matches = 237
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                   51
31%
21
CGAAGCAATGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                             Initial Score = Residue Identity = Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTTG-----
                                                                                                                                                                                                                                                                                                                 CANNCC
.730
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960 970 980 990 1000 1010 1020 1030 GCT-CTTGGTCGCCTCAAGACTGTGCAGGCCCAGCCCGATGGTGTAGGAGTTCTGGAAACAGTGTGCGGGCT
                                     CNINCTTTCTCNACCCCCCCCCTTTTTCATCCCANCGCNAATGGGGTCTCCCCNNCGANGGGGGGNNNCC
                                                                                                                                                                                                                                                                                                                         220 230 240 250 260 x 270 280
TGAGCATGAGGGATTTAAAGGCTTTGGGTAATGGGAACACGATCATACATTCATCATTGTGACCTGCACAC
                                                                                                                                                                                                                                                                                                                                                                                  ACAAGGGGCATAATGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCCTGGGAGGCTCCAGAGGCGCACCTTTCACTACAACAGGAGAAATGAATTTGTGAGGGGAGTACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGGNAGATTTTAAAGAAGGAAAAAAAAAAAAAAAAGGCCCTGAACAGAATTTTCCTGNACAAGGGGCTTCAAA
30 40 50 60 70 80 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 440 450 460 470 480. 490
GAAGCAGGAAATCTCAATTCAGTGAGATAACTGGA-TACCAAGATGATGGTTGAGGCCAAGTGACGCTAATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 510 520 530 540 550 560
ACCTAAACATCGGCATGGTTAGATAGACAGCACAGTCAACACAGTAATCATGATAGTCTGACTTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 580 590 600 610 620 630 640 GAACTATGGTGCTGGCTAGTTGATGATGACCCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------
                                                                                                                                                                                                                                                                   Significance
Mismatches
                                                                                               X 1050 1060 1070 1080 GACAGCACCAGCAGCAGAACAATTCGTTTTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24. US-09-030-606-177' (1-1119)
US-08-904-809-47 Sequence 47, Application US/08904809
                                                                                                                                                                                                                                                           Optimized Score = 256
Matches = 295
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                          310
                                                                                                                                                                                                                                                           50
37%
22
                                                                                                                                                                                                                                                               11 11
                                                                                                                                                                                                                                                          Initial Score
Residue Identity
Gaps
                                                                                                                                            CANNCC
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us-09-030-606-177-inv.res

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650 660 670 680 690 700 710  ATGCAGCAGGACGTCCTTGCACTGGAAGTTGCCGAAATGGTACAACCCTGCCAGGGTTGGGAAAGCTTCTCA	720 730 740 750 760 770 780 CACTCCCAGCCTCCCACAGCATCACAGCATCACAGCCAGC	790 800 810 820 830 840 850  ACGAGGCAAGAGTTCCCCGCGGTAGGGCACTGCGAAGCAATGCTGATGCTCCGGATGGTGTCAGACTCGGAC	860         870         880         890         910         920           ACGGATTCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	930 940 950 960 970 980 990 990 GAGAGGCTC-GCCTCCACCCCGCCCGAGCCTCCAGCCCCGCCCGAGCCTCTGGTCGGCCTCAAGACTGTGCAGGCCCCGGAGCCCTCAAGACTTGCCAGCCCGAGCCTGCTGCCTGC	1000         1010         1020         1030         1040         x         1050         1070           TGGTGTGCGGCTGACAGCACCCCACTGCGGATGCACCAGGACGCCCGAGCAGA           1   1   1   1   1   1   1   1   1   1	1080 1090 ACAATTCGTTTTCCATGACCAGT	25. US-09-030-606-177' (1-1119) US-09-020-747-47 Sequence 47, Application US/09020747	Initial Score = 50 Optimized Score = 256 Significance = 1.65 Residue Identity = 37% Matches = 295 Mismatches = 470 Gaps = 22 Conservative Substitutions = 0	220 230 240 250 250 x 270 280  TGAGCATGAGGGATTTAAAGGCTTTGGGTAATGGGAACACGATCATCATTCAT	290         30         340         350           CACCCTGGGAGGCTCCAGAGGGGCGCCCTTTCACTACAACAGGAGAAATGAATTGTGAGGGGAGTACCAGC         1   1   1   1   1   1   1   1   1   1	360 370 380 400 410 420  ATCCTTGAAGAGCTATATGATCCCTCACCTCTGTAGGTCAGAAATTATGTGGGA-ATGGCTGACACT	430       450       460       470       480       490         GAAGCAGGAAATCTCAATTCAGTGATAACTGGA-TACCAAGTGATGGTTGAGGCCAAGTGACGCTAATTTC

ACAATTCGTTTTCCATGACCAGT

540

530

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